GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 13:53:33 ; Search time 1578.87 Seconds
(without alignments)
603.944 Million cell updates/sec

Title: US-09-802-445-1
Perfect score: 22
Sequence: 1 tgactgtgaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	22	6	BD228690	BD228690 Methods a
2	22	100.0	22	6	BD233617	BD233617 Immunosti
3	22	100.0	22	6	BD251283	BD251283 Enhanceme
4	22	100.0	22	6	BD272057	BD272057 Use of st
5	22	100.0	22	6	AR268334	AR268334 Sequence
6	22	100.0	22	6	AR287741	AR287741 Sequence
7	22	100.0	22	6	AR287743	AR287743 Sequence
8	22	100.0	22	6	AR308057	AR308057 Sequence
9	22	100.0	22	6	AR352573	AR352573 Sequence
10	22	100.0	22	6	AR383158	AR383158 Sequence
11	22	100.0	22	6	AR392162	AR392162 Sequence
12	22	100.0	22	6	AX036945	AX036945 Sequence
13	22	100.0	22	6	AX046993	AX046993 Sequence
14	22	100.0	22	6	AX083675	AX083675 Sequence
15	22	100.0	22	6	AX135650	AX135650 Sequence
16	22	100.0	22	6	AX148636	AX148636 Sequence
17	22	100.0	22	6	AX250701	AX250701 Sequence
18	22	100.0	22	6	AX252291	AX252291 Sequence
19	22	100.0	22	6	AX252509	AX252509 Sequence
20	22	100.0	22	6	AX252520	AX252520 Sequence
21	22	100.0	22	6	AX252934	AX252934 Sequence
22	22	100.0	22	6	AX253113	AX253113 Sequence
23	22	100.0	22	6	AX253123	AX253123 Sequence
24	22	100.0	22	6	AX468499	AX468499 Sequence
25	22	100.0	22	6	AX592312	AX592312 Sequence
26	22	100.0	22	6	AX592350	AX592350 Sequence
27	22	100.0	22	6	AX592369	AX592369 Sequence
28	22	100.0	22	6	AX720306	AX720306 Sequence
29	22	100.0	22	6	BD009235	BD009235 Immunosti
30	22	100.0	22	6	BD182369	BD182369 Anti-tumo
31	22	100.0	22	6	BD185615	BD185615 Anti-tumo
32	22	100.0	22	6	BD190435	BD190435 Microemul
33	21.2	96.4	22	6	AX250707	AX250707 Sequence
34	21	95.5	22	6	BD233630	BD233630 Immunosti
35	21	95.5	22	6	AR352586	AR352586 Sequence
36	21	95.5	22	6	AX083681	AX083681 Sequence
37	21	95.5	22	6	AX148642	AX148642 Sequence
38	21	95.5	22	6	AX252297	AX252297 Sequence
39	21	95.5	22	6	AX252515	AX252515 Sequence
40	21	95.5	22	6	AX252526	AX252526 Sequence
41	21	95.5	22	6	AX252940	AX252940 Sequence
42	21	95.5	22	6	AX253119	AX253119 Sequence
43	21	95.5	22	6	AX253129	AX253129 Sequence
44	21	95.5	22	6	AX592341	AX592341 Sequence
45	21	95.5	22	6	AX592347	AX592347 Sequence

ALIGNMENTS

RESULT 1
BD228690
LOCUS BD228690 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and adjuvants for stimulating mucosal immunity.
ACCESSION BD228690
VERSION BD228690.1 GI:33038460
KEYWORDS JP 2002526425-A/19.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Raz,E., Horner,A.A. and Carson,D.A.
TITLE Methods and adjuvants for stimulating mucosal immunity
JOURNAL Patent: JP 2002526425-A 19 20-AUG-2002;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

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COMMENT     OS   Artificial Sequence
            PN   JP 2002526425-A/19
            PD   20-AUG-2002
            PF   15-SEP-1999 JP 2000573397
            PR   05-OCT-1998 US    09/167039
            PI   EYAL RAZ,ANTHONY A HORNER,DENNIS A CARSON
            PC   A61K39/39,A61K31/7088,A61K31/7105,A61K31/711,A61P11/00 PC
            ,A61P27/14,A61P37/04,
            PC   C12N15/09,G01N33/15,G01N33/50//C12N5/10,G01N33/531,C12N15/00,
            PC   C12N5/00
            CC   non-coding oligonucleotides
            FH   Key             Location/Qualifiers
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FEATURES            Location/Qualifiers
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  Best Local Similarity  100.0%;  Pred. No. 0.41;
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Qy          1 TGACTGTGAACGTTCGAGATGA 22
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Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 2
BD233617
LOCUS       BD233617                  22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Immunostimulatory oligonucleotides, compositions thereof and
            methods of use thereof.
ACCESSION   BD233617
VERSION     BD233617.1  GI:33043387
KEYWORDS    JP 2002517156-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Schwartz,D., Roman,M., Dina,D. and Raz,E.
  TITLE     Immunostimulatory oligonucleotides, compositions thereof and
            methods of use thereof
  JOURNAL   Patent: JP 2002517156-A 2 11-JUN-2002;
            DYNAVAX TECHNOLOGIES CORP
COMMENT     OS   Unidentified
            PN   JP 2002517156-A/2
            PD   11-JUN-2002
            PF   05-JUN-1998 JP 1999502884
            PR   06-JUN-1997 US    60/048793
            PI   DAVID SCHWARTZ,MARK ROMAN,DINO DINA,EYAL RAZ
            PC
            C12N15/09,A61K31/7088,A61K31/7115,A61P37/02,A61P43/00,C12Q1/68, PC
             C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Immunostimulatory oligonucleotides, compositions thereof and
            CC            methods of
            CC   use thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .22
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FEATURES            Location/Qualifiers
     source         1. .22
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ORIGIN

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Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 3
BD251283
LOCUS       BD251283                  22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Enhancement of Neisseria antigen bactericidal activity using CG
            motif-containing oligonucleotide.
ACCESSION   BD251283
VERSION     BD251283.1  GI:33061053
KEYWORDS    JP 2002537353-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Grandi,G., Rappuoli,R., Giuliani,M.M. and Pizza,M.
  TITLE     Enhancement of Neisseria antigen bactericidal activity using CG
            motif-containing oligonucleotide
  JOURNAL   Patent: JP 2002537353-A 19 05-NOV-2002;
            CHIRON SPA
COMMENT     OS   Artificial Sequence
            PN   JP 2002537353-A/19
            PD   05-NOV-2002
            PF   09-FEB-2000 JP 2000600685
            PR   26-FEB-1999 US    60/121792
            PI   GUIDO GRANDI,RINO RAPPUOLI,MARZIA MONICA GIULIANI,MARIAGRAZIA
            PI   PIZZA
            PC   A61K39/095,A61K31/7088,A61K39/39,A61P31/04//C07K14/22,C12N15/
            PC   09,C12N15/00
            CC   oligonucleotide adjuvant
            FH   Key             Location/Qualifiers
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FEATURES            Location/Qualifiers
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  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
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Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 4
BD272057
LOCUS       BD272057                  22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Use of stabilized oligonucleotide for producing agents having
            antitumor activity.
ACCESSION   BD272057
VERSION     BD272057.1  GI:33081825
KEYWORDS    JP 2002539265-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Carpentier,A.
  TITLE     Use of stabilized oligonucleotide for producing agents having
            antitumor activity
  JOURNAL   Patent: JP 2002539265-A 2 19-NOV-2002;
            ASSISTANCE PUBLIQUE HOPITAUX DE PARIS, INSTITUT NATIONAL DE LA
            SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
COMMENT     OS   Artificial Sequence
            PN   JP 2002539265-A/2
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            PD   19-NOV-2002
            PF   17-MAR-2000 JP 2000606246
            PR   19-MAR-1999 FR     99/03433
            PI   ANTOINE CARPENTIER
            PC   A61K47/48,A61K31/711,A61P35/00
            CC   Description of the Artificial Sequence: oligodeoxynucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .22
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FEATURES             Location/Qualifiers
     source          1. .22
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  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 5
AR268334
LOCUS       AR268334                  22 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 19 from patent US 6498148.
ACCESSION   AR268334
VERSION     AR268334.1  GI:29698684
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E.
  TITLE     Immunization-free methods for treating antigen-stimulated
            inflammation in a mammalian host and shifting the host's antigen
            immune responsiveness to a Th1 phenotype
  JOURNAL   Patent: US 6498148-A 19 24-DEC-2002;
FEATURES             Location/Qualifiers
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  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
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Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 6
AR287741
LOCUS       AR287741                  22 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1 from patent US 6534062.
ACCESSION   AR287741
VERSION     AR287741.1  GI:31674761
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E., Cho,H.J., Richman,D. and Horner,A.A.
  TITLE     Methods for increasing a cytotoxic T lymphocyte response in vivo
  JOURNAL   Patent: US 6534062-A 1 18-MAR-2003;
FEATURES             Location/Qualifiers
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Qy          1 TGACTGTGAACGTTCGAGATGA 22
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Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 7
AR287743
LOCUS       AR287743                  22 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3 from patent US 6534062.
ACCESSION   AR287743
VERSION     AR287743.1  GI:31674763
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E., Cho,H.J., Richman,D. and Horner,A.A.
  TITLE     Methods for increasing a cytotoxic T lymphocyte response in vivo
  JOURNAL   Patent: US 6534062-A 3 18-MAR-2003;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 TGACTGTGAACGTTCGAGATGA 22
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Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 8
AR308057
LOCUS       AR308057                  22 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1 from patent US 6552006.
ACCESSION   AR308057
VERSION     AR308057.1  GI:31698950
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E., Kornbluth,R., Catanzaro,A., Hayashi,T. and Carson,D.
  TITLE     Immunomodulatory polynucleotides in treatment of an infection by an
            intracellular pathogen
  JOURNAL   Patent: US 6552006-A 1 22-APR-2003;
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Qy          1 TGACTGTGAACGTTCGAGATGA 22
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Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 9
AR352573
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LOCUS       AR352573                 22 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 2 from patent US 6589940.
ACCESSION   AR352573
VERSION     AR352573.1  GI:33757824
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E., Roman,M. and Dina,D.
  TITLE     Immunostimulatory oligonucleotides, compositions thereof and
            methods of use thereof
  JOURNAL   Patent: US 6589940-A 2 08-JUL-2003;
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RESULT 10
AR383158
LOCUS       AR383158                 22 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6610661.
ACCESSION   AR383158
VERSION     AR383158.1  GI:40092605
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Carson,D.A., Raz,E. and Roman,M.
  TITLE     Immunostimulatory polynucleotide/immunomodulatory molecule
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  JOURNAL   Patent: US 6610661-A 1 26-AUG-2003;
FEATURES             Location/Qualifiers
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Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 11
AR392162
LOCUS       AR392162                 22 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6613751.
ACCESSION   AR392162
VERSION     AR392162.1  GI:40116139
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E. and Rachmilewitz,D.
  TITLE     Method for treating inflammatory bowel disease and other forms of
            gastrointestinal inflammation
  JOURNAL   Patent: US 6613751-A 1 02-SEP-2003;
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RESULT 12
AX036945
LOCUS       AX036945                 22 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 2 from Patent FR2790955.
ACCESSION   AX036945
VERSION     AX036945.1  GI:11226373
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Carpentier,A.
  JOURNAL   Patent: FR 2790955-A 2 22-SEP-2000;
            ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES             Location/Qualifiers
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Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 13
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LOCUS       AX046993                 22 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 2 from Patent WO0067787.
ACCESSION   AX046993
VERSION     AX046993.1  GI:11876420
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Moss,R.B.
  TITLE     Hiv immunogenic compositions and methods
  JOURNAL   Patent: WO 0067787-A 2 16-NOV-2000;
            THE IMMUNE RESPONSE CORPORATION (US)
FEATURES             Location/Qualifiers
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RESULT 14
AX083675
LOCUS       AX083675                  22 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 1 from Patent WO0112223.
ACCESSION   AX083675
VERSION     AX083675.1  GI:13185407
KEYWORDS    .
SOURCE      synthetic construct
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            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of modulating an immune response using immunostimulatory s
            equences and compositions for use therein
  JOURNAL   Patent: WO 0112223-A 1 22-FEB-2001;
            Dynavax Technologies Corporation (US)
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Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 15
AX135650
LOCUS       AX135650                  22 bp    DNA     linear   PAT 29-MAY-2001
DEFINITION  Sequence 21 from Patent WO0132877.
ACCESSION   AX135650
VERSION     AX135650.1  GI:14271920
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mackichan,M.L.
  TITLE     Cpg receptor (cpg-r) and methods relating thereto
  JOURNAL   Patent: WO 0132877-A 21 10-MAY-2001;
            CHIRON CORPORATION (US)
FEATURES             Location/Qualifiers
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  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 16
AX148636
LOCUS       AX148636                  22 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 1 from Patent WO0135991.
ACCESSION   AX148636
VERSION     AX148636.1  GI:14347254
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tuck,S. and van Nest,G.
  TITLE     Immunomodulatory compositions containing an immunostimulatory
            sequence linked to antigen and methods of use thereof
  JOURNAL   Patent: WO 0135991-A 1 25-MAY-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 17
AX250701
LOCUS       AX250701                  22 bp    DNA     linear   PAT 06-OCT-2001
DEFINITION  Sequence 1 from Patent WO0168078.
ACCESSION   AX250701
VERSION     AX250701.1  GI:15984439
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of suppressing hepatitis virus infection using
            immunomodulatory polynucleotide sequences
  JOURNAL   Patent: WO 0168078-A 1 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 18
AX252291
LOCUS       AX252291                  22 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 1 from Patent WO0168117.
ACCESSION   AX252291
VERSION     AX252291.1  GI:15985632
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
```

```
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of reducing papillomavirus infection using immunomodulatory
            polynucleotide sequences
  JOURNAL   Patent: WO 0168117-A 1 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 19
AX252509
LOCUS       AX252509                  22 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 1 from Patent WO0168103.
ACCESSION   AX252509
VERSION     AX252509.1  GI:15985780
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of ameliorating symptoms of herpes infection using
            immunoodulatory polynucleotide sequences
  JOURNAL   Patent: WO 0168103-A 1 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 20
AX252520
LOCUS       AX252520                  22 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 1 from Patent WO0168144.
ACCESSION   AX252520
VERSION     AX252520.1  GI:15985791
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G. and Tuck,S.
  TITLE     Biodegradable immunomodulatory formulations and methods for use
            thereof
  JOURNAL   Patent: WO 0168144-A 1 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 21
AX252934
LOCUS       AX252934                  22 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 1 from Patent WO0168143.
ACCESSION   AX252934
VERSION     AX252934.1  GI:15986201
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G. and Tuck,S.
  TITLE     Immunomodulatory formulations and methods for use thereof
  JOURNAL   Patent: WO 0168143-A 1 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 22
AX253113
LOCUS       AX253113                  22 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 1 from Patent WO0168116.
ACCESSION   AX253113
VERSION     AX253113.1  GI:15986281
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of preventing and treating respiratory viral infeciton usi
            ng immunomodulatory polynucleotide sequences
  JOURNAL   Patent: WO 0168116-A 1 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
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  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 23
AX253123
LOCUS       AX253123                  22 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 1 from Patent WO0168077.
ACCESSION   AX253123
VERSION     AX253123.1  GI:15986291
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of preventing and treating viral infections using
            immunodulatory polynucleotide sequences
  JOURNAL   Patent: WO 0168077-A 1 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match            100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 24
AX468499
LOCUS       AX468499                  22 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 19 from Patent WO0226209.
ACCESSION   AX468499
VERSION     AX468499.1  GI:21901329
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   O'Hagan,D., Otten,G., Donnelly,J.J., Polo,J.M., Barnett,S.,
            Singh,M., Ulmer,J. and Dubensky,T.W.
  TITLE     Microparticles for delivery of the heterologous nucleic acids
  JOURNAL   Patent: WO 0226209-A 19 04-APR-2002;
            CHIRON CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Artificial sequence is synthesized"
ORIGIN

  Query Match            100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 25
AX592312
LOCUS       AX592312                  22 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 2 from Patent WO02052002.
ACCESSION   AX592312
VERSION     AX592312.1  GI:27950414
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 2 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match            100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 26
AX592350
LOCUS       AX592350                  22 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 40 from Patent WO02052002.
ACCESSION   AX592350
VERSION     AX592350.1  GI:27950452
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 40 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match            100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 27
AX592369
LOCUS       AX592369                  22 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 59 from Patent WO02052002.
ACCESSION   AX592369
VERSION     AX592369.1  GI:27950471
KEYWORDS    .
SOURCE      synthetic construct
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  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 59 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 28
AX720306
LOCUS       AX720306                 22 bp    DNA     linear   PAT 15-APR-2003
DEFINITION  Sequence 1 from Patent WO03000232.
ACCESSION   AX720306
VERSION     AX720306.1  GI:29892140
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barenholz,Y., Kedar,E., Louria-Hayon,Y., Joseph,A., Raz,E. and
            Takabayashi,K.
  TITLE     Method for preparation of vesicles loaded with immunostimulatory
            oligodeoxynucleotides
  JOURNAL   Patent: WO 03000232-A 1 03-JAN-2003;
            Yissum Research Development Company of the Hebrew Univ of Jerusalem
            (IL) ; The Regents of the University of California (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 29
BD009235
LOCUS       BD009235                 22 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Immunostimulatory polynucleotide/immunomodulatory molecule
            conjugates.
ACCESSION   BD009235
VERSION     BD009235.1  GI:18637608
KEYWORDS    JP 2001503254-A/34.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Carson,D.A., Raz,E. and Roman,M.
  TITLE     Immunostimulatory polynucleotide/immunomodulatory molecule
  JOURNAL   Patent: JP 2001503254-A 34 13-MAR-2001;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT     OS   Artificial Sequence
            PN   JP 2001503254-A/34
            PD   13-MAR-2001
            PF   09-OCT-1997 JP 1998518649
            PR   11-OCT-1996 US    60/028118
            PI   DENNIS A CARSON,EYAL RAZ,MARK ROMAN
            PC   A61K39/00,A61K39/385,A61K39/39
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 30
BD182369
LOCUS       BD182369                 22 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Anti-tumor antigens or their epitopes against HTLV-1 tumor.
ACCESSION   BD182369
VERSION     BD182369.1  GI:30793287
KEYWORDS    WO 02090981-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hanabuchi,S., Ohashi,T. and Kannagi,M.
  TITLE     Anti-tumor antigens or their epitopes against HTLV-1 tumor
  JOURNAL   Patent: WO 02090981-A 1 14-NOV-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP,SHINO HANABUCHI,TAKASHI OHASHI,
            MARI KANNAGI
COMMENT     OS   Artificial Sequence
            PN   WO 02090981-A/1
            PD   14-NOV-2002
            PF   02-MAY-2002 WO 2002JP004406
            PR   08-MAY-2001 JP 01P   137526
            PI   SHINO HANABUCHI,TAKASHI OHASHI,MARI KANNAGI
            PC   G01N33/50,G01N33/15,A61K39/00
            CC   Description of Artificial Sequence:ISS-ODN
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 31
BD185615
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LOCUS       BD185615                 22 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Anti-tumor antigens or their epitopes against HTLV-I tumor.
ACCESSION   BD185615
VERSION     BD185615.1  GI:31877815
KEYWORDS    JP 2002372532-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hanabuchi,S., Ohashi,T. and Kannagi,M.
  TITLE     Anti-tumor antigens or their epitopes against HTLV-I tumor
  JOURNAL   Patent: JP 2002372532-A 1 26-DEC-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002372532-A/1
            PD   26-DEC-2002
            PF   08-MAY-2001 JP 2001137526
            PI   SHINO HANABUCHI,TAKASHI OHASHI,MARI KANNAGI
            PC   G01N33/50,A61K39/00,A61K39/21,A61P35/00,A61P35/02,A61P37/04,
            PC   C07K7/06,
            PC   C12N5/06,C12Q1/02,G01N33/00,G01N33/15,G01N33/53,G01N33/53, PC
             G01N33/566,
            PC   G01N33/574
            CC   Description of Artificial Sequence:ISS-ODN
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 32
BD190435
LOCUS       BD190435                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Microemulsions with Adsorbed Macromoelecules and Microparticles.
ACCESSION   BD190435
VERSION     BD190435.1  GI:33000174
KEYWORDS    JP 2002537102-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Barackman,J., Simph,M., Ugozoli,M., Kazazu,J., Donnelly,J.,
            Ott,G.S. and Ohagan,D.
  TITLE     Microemulsions with Adsorbed Macromoelecules and Microparticles
  JOURNAL   Patent: JP 2002537102-A 19 05-NOV-2002;
            Chiron Corporation
COMMENT     OS   Artificial Sequence
            PN   JP 2002537102-A/19
            PD   05-NOV-2002
            PF   09-FEB-2000 JP 2000600618
            PR   29-JUL-1999 US    60/146391,28-OCT-1999 US    60/161997, PR
            26-FEB-1999 US    60/121858
            PI   john barackman,manmohan simph,mildred ugozoli,jina kazazu,john

            PI   donnelly,
            PI   gary s ott,derek ohagan
            CC   Oligonucleotide
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 33
AX250707
LOCUS       AX250707                 22 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 7 from Patent WO0168078.
ACCESSION   AX250707
VERSION     AX250707.1  GI:15984445
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of suppressing hepatitis virus infection using
            immunomodulatory polynucleotide sequences
  JOURNAL   Patent: WO 0168078-A 7 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="B is 5-bromocytosine"
ORIGIN

  Query Match             96.4%;  Score 21.2;  DB 6;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 1.2;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||:||||||||||
Db          1 TGACTGTGAABGTTCGAGATGA 22


RESULT 34
BD233630
LOCUS       BD233630                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Immunostimulatory oligonucleotides, compositions thereof and
            methods of use thereof.
ACCESSION   BD233630
VERSION     BD233630.1  GI:33043400
KEYWORDS    JP 2002517156-A/15.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Schwartz,D., Roman,M., Dina,D. and Raz,E.
  TITLE     Immunostimulatory oligonucleotides, compositions thereof and
            methods of use thereof
  JOURNAL   Patent: JP 2002517156-A 15 11-JUN-2002;
            DYNAVAX TECHNOLOGIES CORP
COMMENT     OS   Unidentified
            PN   JP 2002517156-A/15
            PD   11-JUN-2002
            PF   05-JUN-1998 JP 1999502884
            PR   06-JUN-1997 US    60/048793
            PI   DAVID SCHWARTZ,MARK ROMAN,DINO DINA,EYAL RAZ
            PC
            C12N15/09,A61K31/7088,A61K31/7115,A61P37/02,A61P43/00,C12Q1/68, PC
             C12N15/00
```

```
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   5-bromocytosine
            FH   Key             Location/Qualifiers
            FT   modified base   11.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             95.5%;  Score 21;  DB 6;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 1.5;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| ||||||||||
Db          1 TGACTGTGAANGTTCGAGATGA 22


RESULT 35
AR352586
LOCUS       AR352586                 22 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 15 from patent US 6589940.
ACCESSION   AR352586
VERSION     AR352586.1  GI:33757837
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E., Roman,M. and Dina,D.
  TITLE     Immunostimulatory oligonucleotides, compositions thereof and
            methods of use thereof
  JOURNAL   Patent: US 6589940-A 15 08-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .22
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match             95.5%;  Score 21;  DB 6;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 1.5;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| ||||||||||
Db          1 TGACTGTGAANGTTCGAGATGA 22


RESULT 36
AX083681
LOCUS       AX083681                 22 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 7 from Patent WO0112223.
ACCESSION   AX083681
VERSION     AX083681.1  GI:13185413
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of modulating an immune response using immunostimulatory s
            equences and compositions for use therein
  JOURNAL   Patent: WO 0112223-A 7 22-FEB-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
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ORIGIN

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  Best Local Similarity   95.5%;  Pred. No. 1.5;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| ||||||||||
Db          1 TGACTGTGAANGTTCGAGATGA 22


RESULT 37
AX148642
LOCUS       AX148642                 22 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 7 from Patent WO0135991.
ACCESSION   AX148642
VERSION     AX148642.1  GI:14347260
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tuck,S. and van Nest,G.
  TITLE     Immunomodulatory compositions containing an immunostimulatory
            sequence linked to antigen and methods of use thereof
  JOURNAL   Patent: WO 0135991-A 7 25-MAY-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
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ORIGIN

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  Best Local Similarity   95.5%;  Pred. No. 1.5;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| ||||||||||
Db          1 TGACTGTGAANGTTCGAGATGA 22


RESULT 38
AX252297
LOCUS       AX252297                 22 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 7 from Patent WO0168117.
ACCESSION   AX252297
VERSION     AX252297.1  GI:15985638
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of reducing papillomavirus infection using immunomodulatory
            polynucleotide sequences
  JOURNAL   Patent: WO 0168117-A 7 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing (5-bromocytosine)G"
     misc_feature    11
                     /note="n = 5-bromocytosine"
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ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| ||||||||||
Db 1 TGACTGTGAANGTTCGAGATGA 22

RESULT 39
AX252515
LOCUS AX252515 22 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 7 from Patent WO0168103.
ACCESSION AX252515
VERSION AX252515.1 GI:15985786
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS van Nest,G.
TITLE Methods of ameliorating symptoms of herpes infection using immunoodulatory polynucleotide sequences
JOURNAL Patent: WO 0168103-A 7 20-SEP-2001;
Dynavax Technologies Corporation (US)
FEATURES Location/Qualifiers
source 1. .22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing (5-bromocytosine)G"
misc_feature 11
/note="n = 5-bromocytosine"
ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| ||||||||||
Db 1 TGACTGTGAANGTTCGAGATGA 22

RESULT 40
AX252526
LOCUS AX252526 22 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 7 from Patent WO0168144.
ACCESSION AX252526
VERSION AX252526.1 GI:15985797
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS van Nest,G. and Tuck,S.
TITLE Biodegradable immunomodulatory formulations and methods for use thereof
JOURNAL Patent: WO 0168144-A 7 20-SEP-2001;
Dynavax Technologies Corporation (US)
FEATURES Location/Qualifiers
source 1. .22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing (5-bromocytosine) G"
misc_feature 11
/note="n = 5-bromocytosine"
ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| ||||||||||
Db 1 TGACTGTGAANGTTCGAGATGA 22

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Job time : 1579.87 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 13:51:28 ; Search time 319 Seconds
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Title: US-09-802-445-1
Perfect score: 22
Sequence: 1 tgactgtgaacgttcgagatga 22

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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	22	2	AAV32079	Aav32079 Nucleotid
2	22	100.0	22	2	AAV80097	Aav80097 Immunomod
3	22	100.0	22	2	AAV80103	Aav80103 Immunomod
4	22	100.0	22	2	AAV80102	Aav80102 Immunomod
5	22	100.0	22	2	AAX36624	Aax36624 ISS-ODN D
6	22	100.0	22	3	AAA14467	Aaa14467 Immunosti
7	22	100.0	22	3	AAA38072	Aaa38072 Immunosti
8	22	100.0	22	3	AAA38071	Aaa38071 Immunosti
9	22	100.0	22	3	AAA38065	Aaa38065 Immunosti
10	22	100.0	22	3	AAA90458	Aaa90458 CpG adjuv
11	22	100.0	22	3	AAA96253	Aaa96253 Sequence
12	22	100.0	22	3	AAZ55876	Aaz55876 Immunomod
13	22	100.0	22	3	AAC64051	Aac64051 Immunosti
14	22	100.0	22	4	AAH20403	Aah20403 CpG motif
15	22	100.0	22	4	AAH43338	Aah43338 Immunomod
16	22	100.0	22	4	AAH73439	Aah73439 Immunomod
17	22	100.0	22	4	AAH75992	Aah75992 Immunomod
18	22	100.0	22	4	AAF77040	Aaf77040 Immunomod
19	22	100.0	22	4	AAF29800	Aaf29800 Cholera t
20	22	100.0	22	4	AAH44109	Aah44109 5' termin
21	22	100.0	22	4	AAC82107	Aac82107 Oligonucl
22	22	100.0	22	4	AAA92377	Aaa92377 CG motif
23	22	100.0	22	4	AAH42533	Aah42533 Phosphoro
24	22	100.0	22	5	AAH41573	Aah41573 Immunosti
25	22	100.0	22	5	AAS14664	Aas14664 Immunosti
26	22	100.0	22	6	ABQ78627	Abq78627 ISS enhan
27	22	100.0	22	6	AAS15592	Aas15592 Immunosti
28	22	100.0	22	6	ABA03833	Aba03833 Immunosti
29	22	100.0	22	6	ABA03844	Aba03844 Immunosti
30	22	100.0	22	6	AAS16337	Aas16337 ISS polyn
31	22	100.0	22	6	AAD24885	Aad24885 Immunosti
32	22	100.0	22	6	AAD21877	Aad21877 Immunosti
33	22	100.0	22	6	ABQ75259	Abq75259 ISS immun
34	22	100.0	22	6	ABQ75153	Abq75153 ISS immun
35	22	100.0	22	6	ABQ75206	Abq75206 ISS immun
36	22	100.0	22	6	ABV73190	Abv73190 Nucleotid
37	22	100.0	22	6	AAS16348	Aas16348 ISS polyn
38	22	100.0	22	6	AAL44504	Aal44504 CpG motif
39	22	100.0	22	6	ABA03856	Aba03856 Immunosti
40	22	100.0	22	7	AAL51531	Aal51531 CTL recog
41	22	100.0	22	7	ACC49936	Acc49936 Human imm
42	22	100.0	22	7	ABZ57964	Abz57964 Immunosti
43	22	100.0	22	7	ABZ77582	Abz77582 Nucleotid
44	22	100.0	22	8	ADB88931	Adb88931 Chimeric
45	22	100.0	22	8	ADB88799	Adb88799 Chimeric

ALIGNMENTS

RESULT 1
AAV32079
ID AAV32079 standard; DNA; 22 BP.
XX
AC AAV32079;
XX
DT 09-SEP-1998 (first entry)
XX
DE Nucleotide sequence of DY1018.
XX
KW DY1018; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;
KW immunisation; anaphylaxis; IgE; retinopathies; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .22
FT /*tag= a
FT /note= "phosphothioate backbone"
XX
PN WO9816247-A1.
XX
PD 23-APR-1998.
XX
PF 09-OCT-1997; 97WO-US019004.
XX
PR 11-OCT-1996; 96US-0028118P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Carson DA, Raz E, Roman M;
XX
DR WPI; 1998-261028/23.
XX
PT New immunomodulatory compositions - comprising an antigen conjugated to a
PT polynucleotide that contains an immunostimulatory sequence.
XX
PS Example 1; Page 36; 69pp; English.
XX
CC This is the nuclectide sequence of DY1018, which is conjugated to beta-
CC gal to form ISS-PN/IMM, comprising an immunomodulatory molecule (IMM),
CC which comprises an antigen conjugated to a polynucleotide (PN) that
CC contains at least one immunostimulatory nucleotide sequence (ISS). The
CC conjugate synergistically boost the magnitude of the host immune response
CC against an antigen to a level greater that the host immune response to
CC either the IMM, antigen or ISS-PN alone. These responses to ISS-PN/IMM

```
CC   conjugates are particularly acute during the important early phase of the
CC   host immune response to an antigen. The ISS-PN/IMM conjugates boost both
CC   humoral (antibody) and cellular (Th1 type) immune responses of the host.
CC   Thus, use of the method to boost the immune responsiveness of a host to
CC   subsequent challenge by a sensitising antigen without immunisation avoids
CC   the risk of Th2-mediated, immunisation-induced anaphylaxis by suppressing
CC   IgE production in response to the antigen challenge. The conjugates can
CC   also be used to combat pathogenic infection and to stimulate therapeutic
CC   angiogenesis to treat conditions in which localised blood flow plays a
CC   significant etiological role, e.g. retinopathies
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 2
AAV80097
ID   AAV80097 standard; DNA; 22 BP.
XX
AC   AAV80097;
XX
DT   12-MAR-1999  (first entry)
XX
DE   Immunomodulatory oligo comprising an ISS sequence.
XX
KW   Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW   ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW   human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW   B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS   Synthetic.
XX
PN   WO9855495-A2.
XX
PD   10-DEC-1998.
XX
PF   05-JUN-1998;   98WO-US011578.
XX
PR   06-JUN-1997;   97US-0048793P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Schwartz D,  Roman M,  Dina D;
XX
DR   WPI; 1999-059898/05.
XX
PT   Immunostimulatory oligonucleotides regulate the immune system - and
PT   contain an immune-stimulating octanucleotide sequence; for treating
PT   cancer, allergic and infectious diseases.
XX
PS   Claim 5; Page 29; 63pp; English.
XX
CC   The invention relates to immunomodulatory oligonucleotides that comprise
CC   at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC   sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC   GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC   patients needing immune regulation, such as those suffering from cancer,
CC   an allergic disease and asthma. They are also used to prevent infectious
CC   diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC   and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC   Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC   Schistosoma. The immunomodulatory sequences are used to screen for human
CC   immunostimulatory activity by incubating macrophage cells and the
CC   oligonucleotide; and determining the relative amount of Th1-biased
CC   cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC   specific claimed examples of such immunomodulatory oligonucleotides
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 3
AAV80103
ID   AAV80103 standard; DNA; 22 BP.
XX
AC   AAV80103;
XX
DT   12-MAR-1999  (first entry)
XX
DE   Immunomodulatory oligo comprising an ISS sequence.
XX
KW   Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW   ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW   human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW   B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    11
FT                    /*tag=  a
FT                    /note= "5-bromocytosine"
XX
PN   WO9855495-A2.
XX
PD   10-DEC-1998.
XX
PF   05-JUN-1998;   98WO-US011578.
XX
PR   06-JUN-1997;   97US-0048793P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Schwartz D,  Roman M,  Dina D;
XX
DR   WPI; 1999-059898/05.
XX
PT   Immunostimulatory oligonucleotides regulate the immune system - and
PT   contain an immune-stimulating octanucleotide sequence; for treating
PT   cancer, allergic and infectious diseases.
XX
PS   Claim 24; Page 30; 63pp; English.
XX
CC   The invention relates to immunomodulatory oligonucleotides that comprise
CC   at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC   sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC   GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC   patients needing immune regulation, such as those suffering from cancer,
CC   an allergic disease and asthma. They are also used to prevent infectious
CC   diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC   and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC   Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC   Schistosoma. The immunomodulatory sequences are used to screen for human
CC   immunostimulatory activity by incubating macrophage cells and the
CC   oligonucleotide; and determining the relative amount of Th1-biased
CC   cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC   specific claimed examples of such immunomodulatory oligonucleotides
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
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  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 4
AAV80102
ID   AAV80102 standard; DNA; 22 BP.
XX
AC   AAV80102;
XX
DT   12-MAR-1999  (first entry)
XX
DE   Immunomodulatory oligo comprising an ISS sequence.
XX
KW   Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW   ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW   human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW   B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    11
FT                    /*tag=  a
FT                    /note= "5-bromocytosine"
XX
PN   WO9855495-A2.
XX
PD   10-DEC-1998.
XX
PF   05-JUN-1998;   98WO-US011578.
XX
PR   06-JUN-1997;   97US-0048793P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Schwartz D,  Roman M,  Dina D;
XX
DR   WPI; 1999-059898/05.
XX
PT   Immunostimulatory oligonucleotides regulate the immune system - and
PT   contain an immune-stimulating octanucleotide sequence; for treating
PT   cancer, allergic and infectious diseases.
XX
PS   Claim 23; Page 30; 63pp; English.
XX
CC   The invention relates to immunomodulatory oligonucleotides that comprise
CC   at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC   sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC   GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC   patients needing immune regulation, such as those suffering from cancer,
CC   an allergic disease and asthma. They are also used to prevent infectious
CC   diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC   and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC   Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC   Schistosoma. The immunomodulatory sequences are used to screen for human
CC   immunostimulatory activity by incubating macrophage cells and the
CC   oligonucleotide; and determining the relative amount of Th1-biased
CC   cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC   specific claimed examples of such immunomodulatory oligonucleotides
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 5
AAX36624
ID   AAX36624 standard; DNA; 22 BP.
XX
AC   AAX36624;
XX
DT   09-JUL-1999  (first entry)
XX
DE   ISS-ODN DY1018 nucleotide sequence.
XX
KW   Antigen-stimulated inflammation; immunostimulatory oligonucleotide;
KW   granulocyte-mediated tissue inflammation; Th2 type immune response;
KW   immune responsiveness modulation; idiopathic hypereosiniphilic syndrome;
KW   cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;
KW   allergic rhinitis; atopic dermatitis; allergic conjunctivitis;
KW   eosinophilic fasciitis; therapy; ss.
XX
OS   Synthetic.
XX
PN   WO9911275-A2.
XX
PD   11-MAR-1999.
XX
PF   04-SEP-1998;   98WO-US018382.
XX
PR   05-SEP-1997;   97US-00927120.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Ray E;
XX
DR   WPI; 1999-312404/26.
XX
PT   Reducing antigen-stimulated granulocyte-mediated inflammation.
XX
PS   Example 2; Page 30; 69pp; English.
XX
CC   This is the ISS-ODN DY1018 nucleotide sequence. The invention relates to
CC   a method for preventing or reducing antigen-stimulated, granulocyte-
CC   mediated tissue inflammation in a mammal, by administering an
CC   immunostimulatory oligonucleotide (ISS-ODN), where: (a) reduction in, or
CC   the absence of, a Th2 type immune response is measured; or (b) there is a
CC   reduction or absence of other clinical signs of inflammation in the host
CC   after antigen challenge. The method is used to reduce or suppress
CC   granulocyte-mediated inflammation in a host tissue, and to modulate the
CC   host's immune responsiveness to an antigen, particularly where the
CC   subject suffers from asthma, nasal polyposis, allergic rhinitis, atopic
CC   dermatitis, allergic conjunctivitis, eosinophilic fasciitis, idiopathic
CC   hypereosiniphilic syndrome, or cutaneous basophil hypersensitivity.
CC   Unlike prior art treatment by antigen immunisation, the method is an
CC   antigen-independent method, and avoids host production of both
CC   interleukin-4 (IL-4), which carries risk of anaphylaxis, and IL-5 which
CC   actually encourages granulocyte adhesion to endothelia
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 6
AAA14467
ID   AAA14467 standard; DNA; 22 BP.
XX
AC   AAA14467;
XX
```

```
DT   21-AUG-2000  (first entry)
XX
DE   Immunostimulatory oligonucleotide (ISS-ODN) DY1018.
XX
KW   Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;
KW   secretory immunoglobulin A production; sIgA; Th1 phenotype; ds.
XX
OS   Synthetic.
XX
PN   WO200020039-A1.
XX
PD   13-APR-2000.
XX
PF   15-SEP-1999;   99WO-US021203.
XX
PR   05-OCT-1998;   98US-00167039.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Raz E,  Horner AA,  Carson DA;
XX
DR   WPI; 2000-303647/26.
XX
PT   Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to an
PT   antigen in a mammalian host through production of secretory
PT   immunoglobulin A.
XX
PS   Claim 8; Page 21; 64pp; English.
XX
CC   The invention relates to a method of inducing mucosal immunity to an
CC   antigen in a mammalian host, including the the production of secretory
CC   immunoglobulin A (sIgA). Immune protection in the mucosa (the principal
CC   site of entry of most foreign antigens) is mediated by mucosa-associated
CC   lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory
CC   cell sub-populations. The primary immune response which characterises the
CC   induction of mucosal immunity to an antigen is sIgA production by
CC   activated B-cells. The method comprises introducing an immunostimulatory
CC   oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the ISS
CC   -ODN includes a core nucleotide sequence. The core nucleotide sequence is
CC   5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific examples of which
CC   are AACGTT, AGCGTC and GACGTT (SEQ ID NOs 1-3). A specific example of an
CC   ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used as an adjuvant with an
CC   antigen for stimulating mucosal immunity. The level of sIgA production
CC   induced in the host is at least 3 times the magnitude of sIgA production
CC   achievable in response to introduction of antigen alone into the mucosal
CC   tissue and is equivalent or greater than the magnitude of sIgA production
CC   achievable in response to introduction of the antigen and cholera toxin
CC   adjuvant into the mucosal tissue. The host immune response is stimulated
CC   to antigen specific IgA production, biased towards the Th1 phenotype
CC   while antigen-induced IgE production is avoided. The adjuvant has little
CC   or no known toxicity in mammals and its efficacy is comparable to that of
CC   cholera toxin which is used as a mucosal adjuvant. The present sequence
CC   represents the immunostimulatory oligonucleotide DY1018
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 7
AAA38072
ID   AAA38072 standard; DNA; 22 BP.
XX
AC   AAA38072;
XX
DT   24-AUG-2000  (first entry)
XX
DE   Immunostimulatory sequence (ISS) #7.
XX
KW   Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
KW   gp120; human immunodeficiency virus; HIV; immune response; infection;
KW   development; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   11
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-Bromocytosine"
FT   modified_base   15
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "5-Bromocytosine"
XX
PN   WO200021556-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US023677.
XX
PR   09-OCT-1998;   98US-0103733P.
PR   07-OCT-1999;   99US-00415186.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Tighe H,  Raz E,  Schwartz D,  Takabayashi K;
XX
DR   WPI; 2000-317846/27.
XX
PT   Anti-HIV composition comprises immunostimulatory polynucleotides and HIV
PT   glycoprotein gp120 useful for modulating, stimulating an immune response
PT   against HIV in an HIV infected individual.
XX
PS   Disclosure; Page 17; 65pp; English.
XX
CC   The present invention relates to an immunostimulatory composition
CC   comprising a human immunodeficiency virus (HIV) antigen, and an
CC   immunomodulatory polynucleotide comprising an immunostimulatory sequence
CC   (ISS). This sequence represents an ISS that can be used in the
CC   composition. An immunostimulatory composition which comprises a gp120
CC   conjugated to an immunomodulatory polynucleotide, or is proximately
CC   associated to it and not conjugated, is used for modulating or
CC   stimulating a specific immune response against gp120 in an individual by
CC   producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC   is also used for suppressing or delaying development of HIV infection in
CC   an individual infected with HIV or an individual at risk of infection
CC   with HIV, respectively. It is also used for treating an individual
CC   infected with HIV in need of immune modulation
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 8
AAA38071
ID   AAA38071 standard; DNA; 22 BP.
XX
AC   AAA38071;
XX
DT   24-AUG-2000  (first entry)
XX
DE   Immunostimulatory sequence (ISS) #7.
```

```
XX
KW   Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
KW   gp120; human immunodeficiency virus; HIV; immune response; infection;
KW   development; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   11
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-Bromocytosine"
XX
PN   WO200021556-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US023677.
XX
PR   09-OCT-1998;   98US-0103733P.
PR   07-OCT-1999;   99US-00415186.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Tighe H,  Raz E,  Schwartz D,  Takabayashi K;
XX
DR   WPI; 2000-317846/27.
XX
PT   Anti-HIV composition comprises immunostimulatory polynucleotides and HIV
PT   glycoprotein gp120 useful for modulating, stimulating an immune response
PT   against HIV in an HIV infected individual.
XX
PS   Disclosure; Page 17; 65pp; English.
XX
CC   The present invention relates to an immunostimulatory composition
CC   comprising a human immunodeficiency virus (HIV) antigen, and an
CC   immunomodulatory polynucleotide comprising an immunostimulatory sequence
CC   (ISS). This sequence represents an ISS that can be used in the
CC   composition. An immunostimulatory composition which comprises a gp120
CC   conjugated to an immunomodulatory polynucleotide, or is proximately
CC   associated to it and not conjugated, is used for modulating or
CC   stimulating a specific immune response against gp120 in an individual by
CC   producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC   is also used for suppressing or delaying development of HIV infection in
CC   an individual infected with HIV or an individual at risk of infection
CC   with HIV, respectively. It is also used for treating an individual
CC   infected with HIV in need of immune modulation
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 22;  DB 3;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 9
AAA38065
ID   AAA38065 standard; DNA; 22 BP.
XX
AC   AAA38065;
XX
DT   24-AUG-2000  (first entry)
XX
DE   Immunostimulatory sequence (ISS) #1.
XX
KW   Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
KW   gp120; human immunodeficiency virus; HIV; immune response; infection;
KW   development; ss.
XX
OS   Synthetic.
XX
PN   WO200021556-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US023677.
XX
PR   09-OCT-1998;   98US-0103733P.
PR   07-OCT-1999;   99US-00415186.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Tighe H,  Raz E,  Schwartz D,  Takabayashi K;
XX
DR   WPI; 2000-317846/27.
XX
PT   Anti-HIV composition comprises immunostimulatory polynucleotides and HIV
PT   glycoprotein gp120 useful for modulating, stimulating an immune response
PT   against HIV in an HIV infected individual.
XX
PS   Claim 3; Page 16; 65pp; English.
XX
CC   The present invention relates to an immunostimulatory composition
CC   comprising a human immunodeficiency virus (HIV) antigen, and an
CC   immunomodulatory polynucleotide comprising an immunostimulatory sequence
CC   (ISS). This sequence represents an ISS that can be used in the
CC   composition. An immunostimulatory composition which comprises a gp120
CC   conjugated to an immunomodulatory polynucleotide, or is proximately
CC   associated to it and not conjugated, is used for modulating or
CC   stimulating a specific immune response against gp120 in an individual by
CC   producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC   is also used for suppressing or delaying development of HIV infection in
CC   an individual infected with HIV or an individual at risk of infection
CC   with HIV, respectively. It is also used for treating an individual
CC   infected with HIV in need of immune modulation
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 22;  DB 3;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 10
AAA90458
ID   AAA90458 standard; DNA; 22 BP.
XX
AC   AAA90458;
XX
DT   10-JAN-2001  (first entry)
XX
DE   CpG adjuvant oligonucleotide, SEQ ID NO:19.
XX
KW   CpG oligonucleotide; CpG motif; adjuvant; microdroplet emulsion;
KW   microemulsion; adsorbent microparticle; vaccine; Th1 immune response;
KW   viral infection; bacterial infection; parasitic infection; HCV; HBV;
KW   hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;
KW   human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;
KW   rabies virus; cholera; diphtheria; tetanus; pertussis;
KW   Helicobacter pylori; Haemophilus influenzae; malaria; ss.
XX
OS   Synthetic.
XX
PN   WO200050006-A2.
XX
PD   31-AUG-2000.
XX
PF   09-FEB-2000; 2000WO-US003331.
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XX
PR   26-FEB-1999;   99US-0121858P.
PR   29-JUL-1999;   99US-0146391P.
PR   28-OCT-1999;   99US-0161997P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   O'hagan D,  Ott GS,  Donnelly J,  Kazzaz J,  Ugozzoli M,  Singh M;
PI   Barackman J;
XX
DR   WPI; 2000-587123/55.
XX
PT   Microemulsion having an adsorbent surface comprising a microdroplet
PT   emulsion consisting of a metabolizable oil and an emulsifying agent which
PT   is a detergent, useful as a vaccine to treat bacterial, viral, and
PT   parasitic infection.
XX
PS   Claim 17; Page 40; 95pp; English.
XX
CC   The invention relates to a microdroplet emulsion (microemulsion) with an
CC   adsorbent surface, and which comprises a metabolisable oil and an
CC   emulsifying agent (a detergent). It also relates to a composition
CC   comprising the microemulsion and a microparticle with an adsorbent
CC   surface, where the microparticle comprises a polymer selected from a
CC   poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a polycaprolactone,
CC   a polyorthoester, a polyanhydride, and a polycyanoacrylate, and a second
CC   detergent. The surface of the microparticles efficiently adsorb
CC   biologically active macromolecules such as DNA, polypeptides, antigens,
CC   hormones, pharmaceuticals, enzymes, mediators of transcription or
CC   translation, metabolic intermediates and adjuvants. Additionally, a
CC   second biologically active molecule may be encapsulated within the
CC   microparticle. The microemulsion can be used in methods of immunising a
CC   host animal, particularly a human, against a viral, bacterial or
CC   parasitic infection, and in methods of increasing a Th1 immune response.
CC   The microemulsions (having the appropriate antigens adsorbed) may be
CC   particularly used as vaccines for hepatitis C virus (HCV), hepatitis B
CC   virus (HBV), herpes simplex virus (HSV), human immunodeficiency virus
CC   (HIV), cytomegalovirus (CMV), influenza virus, and rabies virus; the
CC   bacteria which cause cholera, diphtheria, tetanus and pertussis;
CC   Helicobacter pylori and Haemophilus influenzae; and malaria-causing
CC   parasites. Sequences AAA90447-A90467 represent Th1 lymphocyte stimulating
CC   oligonucleotides containing at least one CpG motif which are claimed for
CC   use as adjuvants in the compositions of the invention
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 11
AAA96253
ID   AAA96253 standard; DNA; 22 BP.
XX
AC   AAA96253;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Sequence of a stabilised oligonucleotide with antitumour activity.
XX
KW   Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
KW   glioblastoma; medullablastoma; neuroblastoma; melanoma; carcinoma; ss.
XX
OS   Synthetic.
XX
PN   WO200056342-A2.
XX
PD   28-SEP-2000.
XX
PF   17-MAR-2000; 2000WO-FR000676.
XX
PR   19-MAR-1999;   99FR-00003433.
XX
PA   (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
PA   (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
PI   Carpentier A;
XX
DR   WPI; 2000-602192/57.
XX
PT   Use of stabilized oligonucleotides as antitumor agents, particularly
PT   against nervous system tumors, have optimal activity and are not toxic.
XX
PS   Example 2; Page 16; 57pp; French.
XX
CC   The present sequence represents a stabilised oligonucleotide which has
CC   antitumour activity. The oligonucleotide comprises an octomer motif of
CC   the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where the pair
CC   X-X is AT, AA, CT or TT. The oligonucleotides are immunostimulatory, and
CC   are not toxic. They may be adapted for use in animals or humans. The
CC   stabilised oligonucleotides are used for treating tumours, of any type
CC   and any degree of anaplasia, particularly human tumours in the peripheral
CC   or central nervous systems, specifically glioblastomas, medullablastomas,
CC   neuroblastomas, melanomas or carcinomas
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 12
AAZ55876
ID   AAZ55876 standard; DNA; 22 BP.
XX
AC   AAZ55876;
XX
DT   10-APR-2000  (first entry)
XX
DE   Immunomodulatory oligonucleotide SEQ ID NO: 1.
XX
KW   Immunomodulation; immunostimulatory sequence; adjuvant;
KW   Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy; asthma;
KW   immunocontraception; ss.
XX
OS   Mus musculus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .22
FT                   /*tag=  a
FT                   /note= "Phosphorothioate linkages"
FT   misc_feature    9. .16
FT                   /*tag=  b
FT                   /note= "Immunostimulatory sequence (ISS)"
XX
PN   WO9962923-A2.
XX
PD   09-DEC-1999.
XX
PF   04-JUN-1999;   99WO-US012538.
XX
PR   05-JUN-1998;   98US-0088310P.
PR   01-JUN-1999;   99US-00324191.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
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```
XX
PI   Schwartz D;
XX
DR   WPI; 2000-105687/09.
XX
PT   Novel immunomodulatory oligonucleotide used to induce a Th1-type immune
PT   response, e.g. to tumor antigens.
XX
PS   Example 1; Page 35; 54pp; English.
XX
CC   Sequences AAZ55876-Z55877 and AAZ55880-Z55886 represent immunomodulatory
CC   oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,
CC   AACGTC, AACGTT, AGCGTC, AGCGCT, AGCGTT, GACGTC, GACGTT, GGCGTT, AACGTTCC
CC   and GACGTTCC). The invention relates to oligonucleotides comprising one
CC   or more ISSs, where the ISS comprises at least one modified cytosine with
CC   an electron-withdrawing moiety at position C-5 or C-6 of the base.
CC   Sequences AAZ55877 and AAZ55880-Z55886 contain ISSs comprising at least
CC   one bromocytosine, whereas sequence AAZ55876 contains an unmodified ISS.
CC   The immunomodulatory oligonucleotides have an adjuvant-like effect; when
CC   formulated with an antigen, the oligonucleotides stimulate production of
CC   Th1-type cytokines, and induce a Th1-type immune response (activation of
CC   cytotoxic T cells), while simultaneously downregulating the Th2-type
CC   response. The Th1 response is particularly effective for control of
CC   viruses and intracellular parasites. The immunomodulatory
CC   oligonucleotides are used, particularly when formulated with an antigen
CC   or a facilitator, for modulating immune responses. Such compositions may
CC   be used in tumour therapy, in treatment of allergy (including asthma),
CC   for inducing a vigorous cellular response (against a virus, bacterium,
CC   fungus or protozoan), and also in contraceptive vaccines based on sperm
CC   antigens
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 13
AAC64051
ID   AAC64051 standard; DNA; 22 BP.
XX
AC   AAC64051;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.
XX
KW   CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;
KW   enhanced antigen presentation; antigen-presenting cell; APC;
KW   T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;
KW   vaccine; ss.
XX
OS   Synthetic.
XX
PN   WO200062787-A1.
XX
PD   26-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009664.
XX
PR   15-APR-1999;   99US-00292278.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Raz E,  Martin-Orozco E;
XX
DR   WPI; 2000-679548/66.
XX
PT   Enhancing antigen-presentation capabilities of T-cells for cancer
PT   immunotherapy, by contacting cells with an immunostimulatory
PT   oligonucleotide.
XX
PS   Example I; Page 18; 42pp; English.
XX
CC   The invention relates to a method of inducing activation of T-cells to
CC   respond to an antigen, comprising contacting antigen-presenting cells
CC   (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs
CC   thus treated have enhanced antigen presenting capabilities compared to
CC   antigen-activated APCs. APCs with enhanced antigen-presentation
CC   capabilities then present the antigen to T-cells. The method is useful
CC   for cancer immunotherapy. The ISS-ODN is used to enhance the tumour
CC   antigen presenting capacity of tumour cells, thereby inducing T-cell
CC   activation, and is therefore useful for treating tumours. Additionally,
CC   tumour cells treated with an ISS-ODN ex vivo are useful as vaccines. ISS-
CC   ODN treated APCs are induced to take up antigen through upregulation of
CC   Fc-receptor expression, to present antigen through upregulation of major
CC   histocompatibility complex (MHC) Class I and II expression and CD1d
CC   expression, to produce co-stimulatory factors (B7 and CD40), to provide
CC   cell-to-cell adhesion through upregulation of intercellular adhesion
CC   molecule (ICAM) expression, and to increase Th1 stimulatory cytokine
CC   production, all at levels greater than that achieved through contact of
CC   APC with antigen alone. The present sequence represents a
CC   phosphorothioate CpG ISS-ODN used in the exemplifications of the
CC   invention
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 14
AAH20403
ID   AAH20403 standard; DNA; 22 BP.
XX
AC   AAH20403;
XX
DT   03-AUG-2001  (first entry)
XX
DE   CpG motif containing oligonucleotide SEQ ID #21.
XX
KW   Immune system stimulator; CpG motif; CpG receptor; CpG-R; antibacterial;
KW   immune response; vaccine adjuvant; tumour immunotherapy; allergy;
KW   anti-inflammatory; cystic fibrosis; sepsis; heart disease; chlamydia;
KW   inflammatory bowel disease; arthritis; multiple sclerosis; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .22
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate internucleoside linkages"
XX
PN   WO200132877-A2.
XX
PD   10-MAY-2001.
XX
PF   01-NOV-2000; 2000WO-US041735.
XX
PR   02-NOV-1999;   99US-0163157P.
PR   24-NOV-1999;   99US-0167389P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Mackichan ML;
```

XX
DR WPI; 2001-343486/36.
XX
PT Novel CpG receptor and nucleic acid molecule encoding the receptor, for
PT modulating immune response and for identifying compounds of therapeutic
PT use which bind and/or modulate the activity of the receptor.
XX
PS Example 1; Page 14; 41pp; English.
XX
CC Unmethylated CG dinucleotide sequences are commonly found in bacterial
CC DNA, and have been found to stimulate the innate immune system. Natural
CC killer and T cells are activated by exposure to oligonucleotides
CC containing CpG motifs. Oligonucleotides containing CpG motifs can be used
CC as adjuvants in vaccines. The present invention relates to a CpG
CC receptor. The CpG receptor contains a Toll homology domain (THD). The
CC Toll receptor family are associated with responses to pathogens. CpG
CC oligonucleotides may act as stimulators of various immune responses. The
CC CpG receptor or cells expressing the receptor are useful for identifying
CC a compound which binds to or modulates an activity of the CpG receptor.
CC The compounds are useful in e.g. vaccine adjuvants promoting cell-
CC mediated immune responses, antibacterials, (e.g. protection from Listeria
CC infection), tumour immunotherapy, allergy treatment, (e.g. suppressing
CC IgE in human PBMC, shifting from Th2 to Th1) and as anti-inflammatory
CC agents (e.g. for use in cystic fibrosis, sepsis, heart disease,
CC chlamydia, inflammatory bowel disease, arthritis and multiple sclerosis).
CC The present sequence represents a CpG motif containing oligonucleotide
CC used in examples demonstrating that CpG oligonucleotides can activate the
CC MAPK pathways and NF-kappaB
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 15
AAH43338
ID AAH43338 standard; DNA; 22 BP.
XX
AC AAH43338;
XX
DT 13-DEC-2001 (first entry)
XX
DE Immunomodulatory polynucleotide 1018.
XX
KW Immunomodulation; inflammation; gastrointestinal tract;
KW ulcerative colitis; Crohn's disease; inflammatory bowel disease;
KW diarrhoea; rectal bleeding; weight loss; colon; weight; lesion; ss.
XX
OS Synthetic.
XX
PN WO200162207-A2.
XX
PD 30-AUG-2001.
XX
PF 22-FEB-2001; 2001WO-US006034.
XX
PR 23-FEB-2000; 2000US-0184256P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Raz E, Rachmilewitz D;
XX
DR WPI; 2001-565393/63.
XX
PT Ameliorating gastrointestinal inflammation e.g. inflammatory bowel
PT disease involves administering an immunomodulatory nucleic acid.
XX
PS Claim 7; Page 28; 58pp; English.
XX
CC The sequences given in AAH43338-48 represent immunomodulatory
CC polynucleotides which may be used to ameliorate inflammation of the
CC gastrointestinal tract by administering a nucleic acid comprising one of
CC these sequences. These polynucleotides all comprise an immunomodulatory
CC nucleotide sequence of 5'-CpG-3' (I). The nucleotides may be used for
CC ameliorating or reducing gastrointestinal inflammation e.g. chronic or
CC acute gastrointestinal inflammation, ulcerative colitis, Crohn's disease
CC caused by inflammatory bowel disease; diarrhoea, rectal bleeding, weight
CC loss; to reduce colon weight and colon lesions; to reduce a colonic
CC inflammation. The immunomodulatory polynucleotides treat inflammatory
CC bowel disease satisfactorily and effectively and have little or no
CC toxicity even at a high dosage of 50000 micro-g. They also reduce the
CC risk of colonic cancer by treating ulcerative colitis
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 16
AAH73439
ID AAH73439 standard; DNA; 22 BP.
XX
AC AAH73439;
XX
DT 01-OCT-2001 (first entry)
XX
DE Immunomodulatory nucleic acid.
XX
KW G3PDH gene; immunomodulatory oligonucleotide; infection; mycobacterium;
KW intracellular pathogen; anti-pathogenic; ss.
XX
OS Unidentified.
XX
PN WO200155341-A2.
XX
PD 02-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US003029.
XX
PR 31-JAN-2000; 2000US-0179353P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Raz E, Kornbluth R, Catanzaro A, Hayashi T, Carson DA;
XX
DR WPI; 2001-483234/52.
XX
PT Treating infection of intracellular pathogen e.g., Mycobacterium, in a
PT subject, involves administering immunomodulatory nucleic acid molecule to
PT inhibit intracellular replication of intracellular pathogen.
XX
PS Example; Page 26; 54pp; English.
XX
CC The present invention describes a method of treating an infection caused
CC by an intracellular pathogen, involving administering to the patient an
CC immunomodulatory nucleic acid and an anti-pathogenic agent. This is
CC particularly useful in the treatment of mycobacterial infections. The
CC present sequence is an immunomodulatory nucleic acid described in the
CC exemplification of the invention
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;

```
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 17
AAH75992
ID   AAH75992 standard; DNA; 22 BP.
XX
AC   AAH75992;
XX
DT   15-NOV-2001  (first entry)
XX
DE   Immunomodulatory oligonucleotide #1.
XX
KW   Immunomodulatory; immunostimulatory; Th1-type immune response;
KW   Th2-type immune response; interferon; idiopathic pulmonary fibrosis;
KW   viral infection; phosphorothioate; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .22
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate oligonucleotide"
XX
PN   WO200168143-A2.
XX
PD   20-SEP-2001.
XX
PF   12-MAR-2001; 2001WO-US007843.
XX
PR   10-MAR-2000; 2000US-0188557P.
PR   09-MAR-2001; 2001US-00802376.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Van Nest G,  Tuck S;
XX
DR   WPI; 2001-582389/65.
XX
PT   Immunomodulatory polynucleotide/microcarrier complexes comprise an
PT   immunostimulatory sequence containing polynucleotide linked to a
PT   nonbiodegradable microcarrier.
XX
PS   Claim 11; Page 49; 61pp; English.
XX
CC   The present invention relates to immunomodulatory polynucleotide/
CC   microcarrier complexes. The complexes comprise an immunostimulatory
CC   sequence (ISS), e.g. the present sequence, linked to a nonbiodegradable
CC   microcarrier provided that if the microcarrier is gold, latex or magnetic
CC   then the linkage is not biotin/avidin. The complex is useful for
CC   modulating an immune response (especially stimulating a Th1-type response
CC   or suppressing a Th2-type response), increasing interferon-gamma
CC   (especially in a patient suffering from idiopathic pulmonary fibrosis),
CC   increasing interferon-alpha (especially in patients suffering from viral
CC   infection) and reducing levels of IgE
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 18
```

```
AAF77040
ID   AAF77040 standard; DNA; 22 BP.
XX
AC   AAF77040;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Immunomodulatory DNA.
XX
KW   Modulate; immune; antigen; immunostimulatory; ds.
XX
OS   Synthetic.
XX
PN   WO200112223-A2.
XX
PD   22-FEB-2001.
XX
PF   18-AUG-2000; 2000WO-US022835.
XX
PR   19-AUG-1999;   99US-0149768P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Van Nest G;
XX
DR   WPI; 2001-211136/21.
XX
PT   Modulating immune response to a second antigen in humans involves
PT   administering an immunostimulatory polynucleotide comprising an
PT   immunostimulatory sequence and a first antigen.
XX
PS   Claim 31; Page 15; 63pp; English.
XX
CC   The present invention relates to modulating an immune response to a
CC   second antigen in an individual, involving administering to the
CC   individual an immunomodulatory polynucleotide comprising an
CC   immunostimulatory sequence (ISS) and a first antigen
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 19
AAF29800
ID   AAF29800 standard; DNA; 22 BP.
XX
AC   AAF29800;
XX
DT   12-APR-2001  (first entry)
XX
DE   Cholera toxin immunostimulatory nucleotide sequence.
XX
KW   Immunostimulatory nucleotide sequence; immune response; cancer;
KW   antibody production; IFNgamma release; CTL activity; Th1 response;
KW   infection; allergy; ds.
XX
OS   Unidentified.
XX
PN   WO200102007-A1.
XX
PD   11-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US018229.
XX
PR   02-JUL-1999;   99US-00347343.
XX
```

PA (REGC) UNIV CALIFORNIA.
XX
PI Raz E, Kobayashi H;
XX
DR WPI; 2001-138066/14.
XX
PT Enhancing immune response against pathogen or antigen associated with
PT infectious diseases, an allergen or cancer, involves administering
PT immunostimulatory nucleotide sequence prior to antigen exposure.
XX
PS Example 1; Page 14; 47pp; English.
XX
CC The present invention describes a method for enhancing an immune response
CC to a substance, comprising administering an immunostimulatory nucleotide
CC sequence to a subject prior to exposure to the substance. This can be
CC used to enhance antibody production, IFNgamma release, CTL activity and
CC Th1 related effects. The method can be used in the prevention and
CC treatment of allergies, cancer and infections
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 20
AAH44109
ID AAH44109 standard; DNA; 22 BP.
XX
AC AAH44109;
XX
DT 12-SEP-2001 (first entry)
XX
DE 5' terminal NH2 group and a 3' terminal rhodamine moiety oligonucleotide.
XX
KW Peptide nucleic acid; intracellular protein delivery; cationic lipid;
KW PNA; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "T has been modified at the 5' terminal with an
FT NH2 group"
FT modified_base 22
FT /*tag= b
FT /mod_base= OTHER
FT /note= "A has been modified at the 3' terminal with
FT rhodamine"
XX
PN WO200143778-A1.
XX
PD 21-JUN-2001.
XX
PF 15-DEC-2000; 2000WO-US033969.
XX
PR 17-DEC-1999; 99US-0172441P.
XX
PA (GENE-) GENE THERAPY SYSTEMS INC.
XX
PI Felgner PL, Zelphati O;
XX
DR WPI; 2001-398080/42.
XX
PT Composition useful for intracellular delivery of a protein, comprises a
PT protein in operative association with a cationic intracellular delivery
PT vehicle comprising a cationic lipid, which is adapted to fuse with a cell
PT membrane.
XX
PS Example 3; Page 18; 33pp; English.
XX
CC The present invention describes a composition (I) for intracellular
CC delivery of a protein, comprising a protein in operative association with
CC a cationic intracellular delivery vehicle comprising a cationic lipid,
CC where the intracellular delivery vehicle is adapted to fuse with a cell
CC membrane, therefore effecting intracellular delivery of the associated
CC protein. also described is a method for delivering a protein to a cell
CC involving providing the protein associated with a cationic lipid in such
CC a manner so as to form an intracellular delivery composition, and
CC contacting the delivery composition with a cell membrane of a cell, such
CC that the cationic lipid forms an association with a cell membrane and
CC delivers the protein into the cell. (I) is useful in the preparation of a
CC medicament for intracellular delivery of a therapeutic or prophylactic
CC protein. (I) is useful for delivering antibodies to intracellular
CC proteins to neutralise their activity, and to introduce therapeutically
CC useful, proteins, peptides or small molecules. (I) is useful for the in
CC vitro or in vivo delivery of antibodies or peptides which block the
CC function of specific intracellular proteins and affect cellular
CC metabolism, cell viability or virus replication. (I) is useful for
CC delivering any protein of interest, including therapeutically useful
CC proteins (e.g. tumour suppressor proteins, cystic fibrosis transmembrane
CC regulator (CFTR), adenosine deaminase (ADA), hexoseaminidase A, peptides,
CC wild type protein counterparts of mutant proteins and cell surface
CC receptors) such as those for cytokines (e.g., interleukins, interferons,
CC colony stimulating factors) and peptide hormones. The present sequence
CC represents a peptide nucleic acid (PNA) oligonucleotide which is used in
CC an example from the present invention for intracellular delivery of
CC proteins
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 21
AAC82107
ID AAC82107 standard; DNA; 22 BP.
XX
AC AAC82107;
XX
DT 07-MAR-2001 (first entry)
XX
DE Oligonucleotide ODNOct DNA SEQ ID NO 2.
XX
KW Immunogenic; human immunodeficiency virus; immunostimulatory sequence;
KW ISS; beta-chemokine; anti-HIV; AIDS; Th1 immune response; primer;
KW HIV-specific cytotoxic T lymphocyte response; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200067787-A2.
XX
PD 16-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US012495.
XX
PR 06-MAY-1999; 99US-0132762P.
PR 25-AUG-1999; 99US-0150667P.
XX
PA (IMMU-) IMMUNE RESPONSE CORP.
XX
PI Moss RB;
XX

DR WPI; 2001-031804/04.
XX
PT Human immunodeficiency virus (HIV) compositions useful for immunizing and
PT inhibiting AIDS in mammals, comprises HIV devoid of outer envelope
PT protein and an immunostimulatory nucleic acid sequence.
XX
PS Example I; Page 26; 64pp; English.
XX
CC This invention describes a novel immunogenic composition (I), comprising
CC a whole-killed human immunodeficiency virus (HIV) devoid of outer
CC envelope protein gp120, an isolated nucleic acid molecule containing an
CC immunostimulatory sequence (ISS) and an adjuvant, which enhances beta-
CC chemokine levels in a mammal. The products of the invention have anti-HIV
CC activity. (I) is useful for immunizing and for inhibiting AIDS in a
CC mammal. The mammal can be a primate such as a human, (HIV seronegative or
CC seropositive humans) or a rodent, in particular the primate is a pregnant
CC mother or an infant. (I) can induce potent Th1 immune responses against a
CC broad spectrum of HIV epitopes and provides a strong HIV-specific
CC cytotoxic T lymphocyte response
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 22
AAA92377
ID AAA92377 standard; DNA; 22 BP.
XX
AC AAA92377;
XX
DT 12-JAN-2001 (first entry)
XX
DE CG motif and CFA containing oligonucleotide SEQ ID NO:19.
XX
KW CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
KW immune response; ss.
XX
OS Neisseria sp.
XX
FH Key Location/Qualifiers
FT modified_base 1. .22
FT /*tag= a
FT /note= "preferably contains at least one phosphorothioate
FT bond"
XX
PN WO200050075-A2.
XX
PD 31-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-IB000176.
XX
PR 26-FEB-1999; 99US-0121792P.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Rappuoli R, Giuliani MM, Pizza M;
XX
DR WPI; 2001-015529/02.
XX
PT Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX
PS Claim 19; Page 9; 39pp; English.
XX
CC The present invention describes an immunogenic composition (I) comprising
CC a Neisseria antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
CC the present invention. (I) is useful for stimulating an immune response
CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 23
AAH42533
ID AAH42533 standard; DNA; 22 BP.
XX
AC AAH42533;
XX
DT 01-OCT-2001 (first entry)
XX
DE Phosphorothioate beta-gal/immunostimulatory oligonucleotide.
XX
KW Anaphylactic hypersensitivity; immunomodulatory nucleic acid; vaccine;
KW anaphylaxis-associated symptom; IgE; histamine; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200145750-A1.
XX
PD 28-JUN-2001.
XX
PF 20-DEC-2000; 2000WO-US035064.
XX
PR 21-DEC-1999; 99US-0171830P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Raz E, Horner AA;
XX
DR WPI; 2001-475812/51.
XX
PT Reducing risk of anaphylactic hypersensitivity response to an allergen in
PT a subject, by administering an immunomodulating nucleic acid molecule
PT comprising a specific sequence.
XX
PS Example 1; Page 22; 39pp; English.
XX
CC The specification describes a method for reducing a symptom associated
CC with anaphylactic hypersensitivity or risk of anaphylactic response in a
CC subject. The method comprises administering to an individual a nucleic
CC acid molecule comprising an immunomodulatory nucleic acid molecule (INA)
CC comprising the sequence 5'-C-G-3' to reduce anaphylaxis-associated
CC symptom. The method is useful for reducing a symptom associated with
CC anaphylactic hypersensitivity, including elevated IgE level, elevated
CC histamine level, constriction of the airways and difficult breathing
CC which can lead to anaphylactic reaction or anaphylactic shock, thereby
CC reducing the risk of death. The present sequence represents a beta-
CC gal/immunostimulatory sequence, which was used as a vaccine to protect
CC against the development of anaphylactic hypersensitivity
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

```
  Query Match            100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 24
AAH41573
ID   AAH41573 standard; DNA; 22 BP.
XX
AC   AAH41573;
XX
DT   24-AUG-2001  (first entry)
XX
DE   Immunostimulatory sequence (ISS) SEQ ID NO:1.
XX
KW   Immunostimulatory sequence; ISS; immunomodulatory; immune response;
KW   antigen; antiallergic; modulation; Th1 lymphocyte stimulation; allergy;
KW   Th1-associated cytokine; Th2 lymphocyte suppression; cytokine; ss.
XX
OS   Synthetic.
XX
PN   WO200135991-A2.
XX
PD   25-MAY-2001.
XX
PF   15-NOV-2000; 2000WO-US031385.
XX
PR   15-NOV-1999;   99US-0165467P.
PR   14-NOV-2000; 2000US-00713136.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Tuck S,  Van Nest G;
XX
DR   WPI; 2001-329209/34.
XX
PT   Populations of conjugate molecules comprising polynucleotide
PT   immunostimulatory sequences polynucleotides and antigens, useful for
PT   controlling immune responses.
XX
PS   Example 1; Page 30; 97pp; English.
XX
CC   The present invention describes immunomodulatory populations ((I) and
CC   (II)) of conjugate molecules (CMs) comprising immunostimulatory sequences
CC   (ISS) of polynucleotides and antigens. The extent of conjugation affects
CC   the immunological properties (e.g. the extent of antigen-specific
CC   antibody formation, including Th1-associated antibody formation) so the
CC   conjugates are used for altering the type and extent of immune response.
CC   (I) and (II) have immunomodulatory, immunosuppressive and antiallergic
CC   activities, and can be used in the modulation of immune responses via the
CC   stimulation of Th1 lymphocytes and Th1-associated cytokines, and
CC   suppression of Th2 lymphocytes and cytokines. The populations ((I) and
CC   (II)) of conjugate molecules may be used for modulating immune responses
CC   in individuals e.g. for the treatment of an allergic condition. (I) and
CC   (II) may be used to modulate immune responses and therefore prevent
CC   potentially harmful reactions to antigens. The present sequence
CC   represents an ISS polynucleotide which is used in the exemplification of
CC   the present invention
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 22;  DB 5;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 25
AAS14664
ID   AAS14664 standard; DNA; 22 BP.
XX
AC   AAS14664;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Immunostimulatory sequence, ISS #1.
XX
KW   Immunostimulatory sequence; ISS; ds; antiviral; immunogen;
KW   respiratory syncytial virus; RSV; influenza virus; rhinovirus;
KW   adenovirus; measles virus; mumps virus; parainfluenza virus;
KW   rubella virus; poxvirus; parvovirus; hantavirus; varicella virus.
XX
OS   Respiratory syncytial virus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .22
FT                   /*tag=  a
FT                   /label= OTHER
FT                   /note= "Phosphorothioate Backbone"
XX
PN   WO200168116-A2.
XX
PD   20-SEP-2001.
XX
PF   12-MAR-2001; 2001WO-US007839.
XX
PR   10-MAR-2000; 2000US-0188583P.
PR   09-MAR-2001; 2001US-00802686.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Van Nest G;
XX
DR   WPI; 2001-607438/69.
XX
PT   Suppressing a respiratory syncytial virus infection by administering an
PT   immunostimulatory sequence at the site of infection is useful to prevent
PT   and treat lower respiratory tract viral infections.
XX
PS   Claim 5; Page 37; 40pp; English.
XX
CC   The invention relates to suppressing a respiratory syncytial virus (RSV)
CC   infection in an exposed individual, comprising administering a
CC   polynucleotide comprising an immunostimulatory sequence (ISS) comprising
CC   the sequence 5'-C, G-3', where an RSV antigen is not administered. The
CC   invention is used to prevent and treat respiratory syncytial virus
CC   infection of the lower respiratory tract and other viruses including
CC   influenza virus, rhinovirus, adenovirus, measles virus, mumps virus,
CC   parainfluenza virus, rubella virus, poxvirus, parvovirus, hantavirus and
CC   varicella virus. A kit for carrying out the administration is also
CC   included. Unlike the prior art antiviral agent ribavirin, which is a
CC   potential teratogen, the invention provides a treatment which does not
CC   carry unacceptable side effects. Other prior art medicaments treat the
CC   symptoms only, whilst the invention treats the infection. The present
CC   sequence is an ISS of the invention
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 22;  DB 5;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22
```

RESULT 26
ABQ78627
ID ABQ78627 standard; DNA; 22 BP.
XX
AC ABQ78627;
XX
DT 25-NOV-2002 (first entry)
XX
DE ISS enhancing HIV-specific Th1 cytokine and humoral responses.
XX
KW Immunostimulatory sequence; ISS; Th1 cytokine response; humoral response;
KW HIV; beta-chemokine; immunisation; AIDS; ss.
XX
OS Unidentified.
XX
PN WO200258726-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002077.
XX
PR 26-JAN-2001; 2001US-0264476P.
XX
PA (IMMU-) IMMUNE RESPONSE CORP.
XX
PI Moss RB, Carlo DJ;
XX
DR WPI; 2002-643331/69.
XX
PT Treating an HIV-infected individual comprises treatment with anti-
PT retroviral compound and immunization with an HIV immunogenic composition
PT with structured cycles of anti-retroviral treatment and withdrawal from
PT treatment.
XX
PS Disclosure; Page 15; 31pp; English.
XX
CC The present sequence represents an exemplary immunostimulatory sequence
CC (ISS) which enhances HIV-specific Th1 cytokine and humoral responses, and
CC also enhances both non-specific and HIV-specific beta-chemokine
CC production. ISSs can be included in HIV immunogenic compositions of the
CC invention. The specification describes a method for treating an HIV-
CC infected individual, which comprises combining immunisation with an anti-
CC retroviral compound, an HIV immunogenic composition with structured
CC cycles of anti-retroviral treatment and withdrawal from treatment. The
CC advantages of the method of the invention include a delay in the rebound
CC to an unacceptably high viral load; a more rapid or sustained increase in
CC HIV-specific CD4 T cell counts; a reduction or delay in the development
CC of AIDS symptoms, including AIDS-related opportunistic infections; and a
CC higher degree of patient compliance with treatment and fewer toxic side
CC effects associated with long-term anti-retroviral drug treatment. The
CC method is useful for treating an HIV-infected individual
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 27
AAS15592
ID AAS15592 standard; DNA; 22 BP.
XX
AC AAS15592;
XX
DT 29-JAN-2002 (first entry)
XX
DE Immunostimulatory oligonucleotide (ISS-ODN) #1.
XX
KW Immunostimulatory oligonucleotide; ISS-ODN; antiallergic; antibacterial;
KW virucide; fungicide; vaccine; immunogen; plant allergen; ragweed;
KW grass pollen; food; latex; cat dander; cockroach; house dust mite;
KW pathogenic parasite; ss.
XX
OS Synthetic.
XX
PN WO200176642-A1.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US011290.
XX
PR 07-APR-2000; 2000US-0195890P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Raz E, Takabayashi K, Nguyen M;
XX
DR WPI; 2002-025886/03.
XX
PT New polynucleotide vaccine for eliciting immune response to an antigen
PT derived from a pathogen, plant or food, comprises antigen-encoding
PT nucleic acid sequence derived from non-host species of first phylum or
PT kingdom.
XX
PS Example 4; Page 43; 64pp; English.
XX
CC The invention relates to a polynucleotide vaccine (I) comprising a
CC nucleic acid sequence encoding an antigen derived from a non-host species
CC of a first phylum or first kingdom, where the nucleic acid sequence
CC encoding the antigen is modified by deletion of a native signal sequence,
CC and/or an immunomodulatory nucleic acid sequence. (I) is useful for
CC modulating an immune response to an antigen, especially a plant (ragweed
CC or grass pollen), food, latex, cat dander, cockroach or house dust mite
CC allergen. (I) is also useful for eliciting an immune response to an
CC antigen derived from a pathogen, such as bacterium, virus or a parasite.
CC The vaccine is co-administered with an immunostimulatory nucleotide
CC sequence which comprises an unmethylated 5'-CG-3' nucleotide sequence.
CC Antigens of pathogenic parasites include Plasmodium, Leishmania, fungal,
CC yeast or other pathogens. The present sequence represents
CC immunostimulatory oligonucleotide (ISS-ODN) #1 which is co-injected with
CC (I) to amplify the immune response to the co-administered allergen
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 28
ABA03833
ID ABA03833 standard; DNA; 22 BP.
XX
AC ABA03833;
XX
DT 12-FEB-2002 (first entry)
XX
DE Immunostimulatory sequence (ISS) SEQ ID NO:1.
XX
KW Immunomodulatory polynucleotide/microcarrier complex; IMP/MC; IgE;
KW immunomodulation; immunostimulation; phosphorothioate; immunomodulator;
KW antiallergic; antibacterial; antiprotozoal; antiparasitic; hepatotropic;
KW nephrotropic; interferon-alpha stimulator; interferon-gamma stimulator;
KW immunoglobulin E stimulator; immune response; IPF; scleroderma; malaria;
KW idiopathic pulmonary fibrosis; cutaneous radiation-induced fibrosis;
KW hepatic fibrosis; renal fibrosis; infectious disease; leishmaniasis;
KW mycobacterial disease; toxoplasmosis; schistosomiasis; chlonorchiasis;

KW allergy; allergy-induced asthma; prophylactic vaccine; cancer; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .22
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages"
XX
PN WO200168144-A2.
XX
PD 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-US007848.
XX
PR 10-MAR-2000; 2000US-0188303P.
PR 09-MAR-2001; 2001US-00802359.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Van Nest G, Tuck S;
XX
DR WPI; 2002-049002/06.
XX
PT New immunomodulatory polynucleotide/microcarrier complex, useful for
PT modulating the immune response of individuals, particularly humans, or
PT for treating idiopathic pulmonary fibrosis, scleroderma, malaria or
PT allergies.
XX
PS Claim 14; Page 49; 63pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide/
CC microcarrier (IMP/MC) complex (I), which comprises a polynucleotide
CC having an immunostimulatory sequence (ISS) linked to a biodegradable
CC microcarrier (MC). The ISS comprises the sequence: 5'-CG-3', where the MC
CC is less than 10 micro m in size. (I) has immunomodulator, antiallergic,
CC antibacterial, antiprotozoal, antiparasitic, hepatotropic and
CC nephrotropic activities. It can be used as an interferon (IFN)-alpha
CC stimulator, IFN-gamma stimulator or an immunoglobulin E (IgE) stimulator.
CC (I) can be used for modulating the immune response of individuals,
CC particularly humans. The IMP/MC complex is particularly useful for
CC treating idiopathic pulmonary fibrosis (IPF), scleroderma, cutaneous
CC radiation-induced fibrosis, hepatic fibrosis including schistosomiasis-
CC induced hepatic fibrosis, renal fibrosis, infectious diseases caused by
CC cellular pathogen (e.g. a mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis or chlonorchiasis), or disorders
CC associated with a Th2-type immune response (e.g. allergies or allergy-
CC induced asthma). The IMP/MC may also be used in individuals receiving
CC therapeutic or prophylactic vaccines, in individuals suffering from
CC cancer, or in individuals at risk of exposure to an infectious agent. The
CC present sequence represents a specifically claimed ISS which can be used
CC in an IMP/MC complex of the present invention
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 29
ABA03844
ID ABA03844 standard; DNA; 22 BP.
XX
AC ABA03844;
XX
DT 12-FEB-2002 (first entry)
XX
DE Immunostimulatory sequence (ISS) SEQ ID NO:1.
XX
KW Immunostimulatory sequence; ISS; immunostimulation; viral infection;
KW immunomodulation; virucide; gene therapy; viraemia; phosphorothioate; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .22
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages"
XX
PN WO200168077-A2.
XX
PD 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-US007840.
XX
PR 10-MAR-2000; 2000US-0188302P.
PR 09-MAR-2001; 2001US-00802685.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Van Nest G;
XX
DR WPI; 2002-048999/06.
XX
PT Reducing severity, recurrence or duration of symptom of virus infection,
PT or reducing viremia or blood levels of virus antigen, comprises
PT administering a polynucleotide having an immunostimulatory sequence.
XX
PS Claim 4; Page 54; 65pp; English.
XX
CC The present invention describes a method for reducing severity of a
CC symptom of virus infection in an individual infected with a virus. The
CC method comprises administering a composition consisting of a
CC polynucleotide having an immunostimulatory sequence (ISS). The ISS
CC comprises the sequence 5'-C,G,pyrimidine,pyrimidine,C,G-3'. An antigen is
CC administered in conjunction with the composition. ISS has virucide
CC activity and can be used in gene therapy. The method using the ISS can be
CC used for suppressing, ameliorating and/or preventing viral infections to
CC an individual who may be at risk of being exposed to, exposed to or
CC infected by a virus. It may also be used in reducing the recurrence or
CC duration of a symptom of viral infection, delaying the development of a
CC virus infection, and reducing viraemia or blood levels of virus antigens.
CC The present sequence represents a specifically claimed ISS for use in the
CC method of the invention
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 30
AAS16337
ID AAS16337 standard; DNA; 22 BP.
XX
AC AAS16337;
XX
DT 14-FEB-2002 (first entry)
XX
DE ISS polynucleotide #1 useful for treating herpes virus infections.
XX
KW Herpes simplex virus; HSV infection; immunostimulatory sequence; ISS;
KW immune response; alphaherpesvirinae; herpes virus zoster virus; VZV;
KW HSV-1; HSV-2; chicken pox; herpes labialis; cold sore; genital herpes;

```
KW   virucide; phosphorothioate; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .22
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Optionally phosphorothioate internucleotide
FT                   linkages"
XX
PN   WO200168103-A2.
XX
PD   20-SEP-2001.
XX
PF   12-MAR-2001; 2001WO-US007841.
XX
PR   10-MAR-2000; 2000US-0188556P.
PR   09-MAR-2001; 2001US-00802518.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Van Nest G;
XX
DR   WPI; 2002-041171/05.
XX
PT   Preventing, reducing the severity or reducing the recurrence of an
PT   infection or symptom of herpes simplex virus (HSV), e.g. HSV-2, comprises
PT   administering an immunostimulatory sequence to an individual.
XX
PS   Claim 5; Page 41; 49pp; English.
XX
CC   The present invention relates to novel methods of treating, preventing,
CC   or reducing the severity or recurrence of a symptom of herpes simplex
CC   virus (HSV) infection in an individual who has been exposed to or who is
CC   infected with HSV. The method comprises administering a polynucleotide
CC   having an immunostimulatory sequence (ISS; AAS16337-AAS16345) which
CC   induces an immune response. A composition containing ISS is administered
CC   without a HSV (alphaherpesvirinae) antigen. The composition can be
CC   included in a kit for ameliorating or preventing a symptom of HSV
CC   infection caused by herpes virus zoster virus (VZV), HSV-1 and
CC   particularly HSV-2. Such HSV infections include chicken pox, herpes
CC   labialis (cold sores) and genital herpes. The present sequence represents
CC   one of the ISS polynucleotides of the invention. Note: The present
CC   sequence is shown as single stranded in the specification, but the
CC   patentees state on page 20 that this sequence may be double stranded
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 31
AAD24885
ID   AAD24885 standard; DNA; 22 BP.
XX
AC   AAD24885;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Immunostimulatory oligodeoxynucleotide (ISS-ODN) 1.
XX
KW   Cell death; DNA damage; DNA-dependent protein kinase; DNA-PK; necrosis;
KW   immune response; apoptosis; Alzheimer's disease; Parkinson's disease;
KW   rheumatoid arthritis; inflammation; osteoporosis; myocardial infarction;
KW   liver disease; reperfusion injury; carcinoma; multiple sclerosis; stroke;
KW   amyotrophic lateral sclerosis; Acquired Immune Deficiency Syndrome; AIDS;
KW   head injury damage; aplastic anaemia; tumour; organ transplantation;
KW   cerebral infarction; follicular lymphomas; systemic lupus erythematosus;
KW   viral infection; glomerulonephritis; apoptosis; autoimmune disorder;
KW   sepsis; immunostimulatory oligodeoxynucleotide; ISS-ODN; ss.
XX
OS   Unidentified.
XX
PN   WO200185910-A2.
XX
PD   15-NOV-2001.
XX
PF   04-MAY-2001; 2001WO-US014508.
XX
PR   05-MAY-2000; 2000US-0202274P.
PR   17-JAN-2001; 2001US-0262321P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Raz E,  Lois AF,  Takabayashi K;
XX
DR   WPI; 2002-062244/08.
XX
PT   Modulating cell death or reducing DNA damage in eukaryotic cells, useful
PT   for reducing cell death in individual or organ, comprises contacting cell
PT   with agent modulating biological activity of DNA-dependent protein
PT   kinase.
XX
PS   Example 1; Page 29; 57pp; English.
XX
CC   The invention relates to a method for modulating cell death or reducing
CC   DNA damage in an eukaryotic cell by contacting the cell with an agent
CC   that modulates the biological activity of DNA-dependent protein kinase
CC   (DNA-PK). The invention also relates nucleic acids which modulate the
CC   immune response binding to Ku antigen, resulting in activation of DNA-PK.
CC   The method is useful for modulating cell death or reducing DNA damage in
CC   an eukaryotic cell, for treating any disorder resulting from a genotoxic
CC   insert to a cell e.g., necrosis, apoptosis. The method is also useful for
CC   treating cell death-related indications such as Alzheimer's disease,
CC   Parkinson's disease, rheumatoid arthritis, septic shock, sepsis, stroke,
CC   central nervous system inflammation, osteoporosis, degenerative liver
CC   disease, cerebellar degeneration, reperfusion injury, multiple sclerosis,
CC   amyotrophic lateral sclerosis, myocardial infarction, head injury damage,
CC   acquired immunodeficiency syndrome (AIDS), aplastic anaemia, cerebral
CC   infarction, bypass heart surgery, organ transplantation. The method is
CC   also useful for treating follicular lymphomas, carcinomas, autoimmune
CC   disorders (systemic lupus erythematosus), hormone dependent tumours,
CC   immune mediated glomerulonephritis; apoptosis and viral infections. The
CC   present sequence is immunostimulatory oligodeoxynucleotide (ISS-ODN) used
CC   for identifying ISS-binding protein, which is used in the exemplification
CC   of the invention
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 32
AAD21877
ID   AAD21877 standard; DNA; 22 BP.
XX
AC   AAD21877;
XX
DT   12-FEB-2002  (first entry)
XX
DE   Immunostimulatory sequence oligonucleotide (ISS-ODN) #1.
XX
KW   Cytotoxic T lymphocyte; CTL; T cell; tumour load; cancer radiotherapy;
```

```
KW   immunostimulatory sequence oligonucleotide; ISS-ODN; chemotherapy;
KW   immunosuppression; transplantation; autoimmune disease; infection;
KW   acquired immune deficiency syndrome; AIDS; intracellular pathogen;
KW   cytomegalovirus; mycobacterial infection; Epstein-Barr virus;
KW   varicella zoster virus; human immunodeficiency virus; HIV;
KW   phosphorothioate backbone; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .22
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
FT   modified_base   1
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Disulphide thymine"
XX
PN   WO200172123-A1.
XX
PD   04-OCT-2001.
XX
PF   28-MAR-2001; 2001WO-US010118.
XX
PR   28-MAR-2000; 2000US-0192537P.
PR   11-MAY-2000; 2000US-0203567P.
PR   05-JUL-2000; 2000US-0215895P.
XX
PA   (REGC ) UNIV CALIFORNIA.
PA   (VETE-) DEPT VETERANS AFFAIRS.
XX
PI   Raz E,  Cho HJ,  Richman DD,  Horner AA;
XX
DR   WPI; 2002-010699/01.
XX
PT   Increasing antigen-specific cytotoxic T lymphocyte activity in a CD4+ T
PT   cell deficient individual, useful to treat immunodeficiency and block HIV
PT   infection, comprises administering immunostimulatory nucleic acid.
XX
PS   Example 1; Page 44; 91pp; English.
XX
CC   The present invention relates to a method for increasing antigen-specific
CC   cytotoxic T lymphocyte (CTL) activity in a CD4+ T cell-deficient
CC   individual, comprising administering an immunostimulatory sequence
CC   oligonucleotide (ISS-ODN). The immunostimulatory nucleic acids of the
CC   invention are used in CD4+ T cell-deficient individuals to decrease
CC   tumour load, to treat a primary or acquired immunodeficiency,
CC   particularly where the acquired immunodeficiency is temporary and due to
CC   cancer radiotherapy or chemotherapy or immunosuppression following bone
CC   marrow or organ transplantation, or autoimmune disease treatment, or is
CC   acquired immunodeficiency syndrome (AIDS). The nucleic acids may be used
CC   to treat a person at risk of becoming CD4+ T cell-deficient, particularly
CC   where someone at risk of cancer recurrence. They are also used to treat
CC   infection, particularly by an intracellular pathogen, especially one
CC   caused by cytomegalovirus, Mycobacterium tuberculosis, M. avium, Epstein-
CC   Barr virus, a fungus yeast, varicella zoster virus or human
CC   immunodeficiency virus (HIV). The present sequence is a 5' disulfide-
CC   linked phosphorothioate immunostimulatory sequence oligonucleotide (ISS-
CC   ODN), used in the exemplification of the invention
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 33
ABQ75259
ID   ABQ75259 standard; DNA; 22 BP.
XX
AC   ABQ75259;
XX
DT   05-NOV-2002  (first entry)
XX
DE   ISS immunomodulatory positive control oligonucleotide SEQ ID NO:59.
XX
KW   Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW   allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW   idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW   malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW   immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW   virucide; antibacterial; protozoacide; ss.
XX
OS   Synthetic.
XX
PN   WO200252002-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-US050821.
XX
PR   27-DEC-2000; 2000US-0258675P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D;
XX
DR   WPI; 2002-657426/70.
XX
PT   Immunomodulatory polynucleotide for modulating an immune response in a
PT   subject suffering from disorders associated with Th2-type immune
PT   response, e.g. allergy, or infectious disease, comprises an
PT   immunostimulatory sequence.
XX
PS   Example 1; Page 71; 95pp; English.
XX
CC   The present invention describes an immunomodulatory polynucleotide (I)
CC   comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC   immunomodulatory composition comprising (I); (2) an immunomodulatory
CC   polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC   biodegradable MC, where the MC is less than 10 micrometre in size; and
CC   (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC   antibacterial and protozoacide activities, and can be used as a modulator
CC   of immune response. (I) is useful for modulating an immune response in an
CC   individual suffering from disorders associated with a Th2-type immune
CC   response, especially an allergy or asthma, or an infectious disease. (I)
CC   is also useful for increasing interferon-gamma (IFN-gamma) in an
CC   individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC   individual having a viral infection. (I) is further useful for
CC   ameliorating a symptom of an infectious disease caused by a cellular
CC   pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC   toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC   symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC   allergy-related disorder, in particular asthma in an individual. The
CC   present sequence represents an immunomodulatory related oligonucleotide
CC   which was used in an example from the present invention
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 34
ABQ75153
```

```
ID   ABQ75153 standard; DNA; 22 BP.
XX
AC   ABQ75153;
XX
DT   05-NOV-2002  (first entry)
XX
DE   ISS immunomodulatory oligonucleotide SEQ ID NO:2.
XX
KW   Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW   allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW   idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW   malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW   immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW   virucide; antibacterial; protozoacide; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        13
FT                   /*tag=  a
FT                   /note= "uracil"
XX
PN   WO200252002-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-US050821.
XX
PR   27-DEC-2000; 2000US-0258675P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D;
XX
DR   WPI; 2002-657426/70.
XX
PT   Immunomodulatory polynucleotide for modulating an immune response in a
PT   subject suffering from disorders associated with Th2-type immune
PT   response, e.g. allergy, or infectious disease, comprises an
PT   immunostimulatory sequence.
XX
PS   Claim 4; Page 20; 95pp; English.
XX
CC   The present invention describes an immunomodulatory polynucleotide (I)
CC   comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC   immunomodulatory composition comprising (I); (2) an immunomodulatory
CC   polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC   biodegradable MC, where the MC is less than 10 micrometre in size; and
CC   (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC   antibacterial and protozoacide activities, and can be used as a modulator
CC   of immune response. (I) is useful for modulating an immune response in an
CC   individual suffering from disorders associated with a Th2-type immune
CC   response, especially an allergy or asthma, or an infectious disease. (I)
CC   is also useful for increasing interferon-gamma (IFN-gamma) in an
CC   individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC   individual having a viral infection. (I) is further useful for
CC   ameliorating a symptom of an infectious disease caused by a cellular
CC   pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC   toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC   symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC   allergy-related disorder, in particular asthma in an individual. The
CC   present sequence represents an immunomodulatory oligonucleotide which is
CC   specifically claimed in the present invention
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 5 T; 1 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.17;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||:|||||||||
Db          1 TGACTGTGAACGUTCGAGATGA 22
```

```
RESULT 35
ABQ75206
ID   ABQ75206 standard; DNA; 22 BP.
XX
AC   ABQ75206;
XX
DT   05-NOV-2002  (first entry)
XX
DE   ISS immunomodulatory oligonucleotide SEQ ID NO:40.
XX
KW   Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW   allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW   idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW   malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW   immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW   virucide; antibacterial; protozoacide; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        14
FT                   /*tag=  a
FT                   /note= "uracil"
XX
PN   WO200252002-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-US050821.
XX
PR   27-DEC-2000; 2000US-0258675P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D;
XX
DR   WPI; 2002-657426/70.
XX
PT   Immunomodulatory polynucleotide for modulating an immune response in a
PT   subject suffering from disorders associated with Th2-type immune
PT   response, e.g. allergy, or infectious disease, comprises an
PT   immunostimulatory sequence.
XX
PS   Disclosure; Page 22; 95pp; English.
XX
CC   The present invention describes an immunomodulatory polynucleotide (I)
CC   comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC   immunomodulatory composition comprising (I); (2) an immunomodulatory
CC   polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC   biodegradable MC, where the MC is less than 10 micrometre in size; and
CC   (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC   antibacterial and protozoacide activities, and can be used as a modulator
CC   of immune response. (I) is useful for modulating an immune response in an
CC   individual suffering from disorders associated with a Th2-type immune
CC   response, especially an allergy or asthma, or an infectious disease. (I)
CC   is also useful for increasing interferon-gamma (IFN-gamma) in an
CC   individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC   individual having a viral infection. (I) is further useful for
CC   ameliorating a symptom of an infectious disease caused by a cellular
CC   pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC   toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC   symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC   allergy-related disorder, in particular asthma in an individual. The
CC   present sequence represents an immunomodulatory oligonucleotide from the
CC   present invention
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 5 T; 1 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.17;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||:|||||||||
Db          1 TGACTGTGAACGTUCGAGATGA 22


RESULT 36
ABV73190
ID   ABV73190 standard; DNA; 22 BP.
XX
AC   ABV73190;
XX
DT   08-JAN-2003  (first entry)
XX
DE   Nucleotide sequence of an immunostimulatory oligonucleotide ISS-1.
XX
KW   Immunomodulator; immunostimulant; antiinflammatory; antiasthmatic; Th2;
KW   antiallergic; dermatological; vaccine; gene therapy; immune response; ss.
XX
OS   Synthetic.
XX
PN   WO200274922-A2.
XX
PD   26-SEP-2002.
XX
PF   15-MAR-2002; 2002WO-US008207.
XX
PR   16-MAR-2001; 2001US-0276865P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Broide DH,  Raz E;
XX
DR   WPI; 2002-740857/80.
XX
PT   Suppressing a symptom of an allergic response in a subject, useful for
PT   preventing inflammation associated with allergy, comprises administering
PT   to an antigen-sensitized host first and second doses of an
PT   immunomodulatory nucleic acid.
XX
PS   Example; Page 27; 98pp; English.
XX
CC   The invention relates to suppressing symptoms of allergic response that
CC   involves administering to an antigen-sensitized mammalian host a dose of
CC   a composition comprising an immunomodulatory nucleic acid, and a second
CC   dose of a composition comprising an immunomodulatory nucleic acid, about
CC   1 day - 8 weeks after the first dose. The immunomodulatory nucleic acid
CC   comprises a nucleotide sequence comprising 5'-CG-3'. The methods are
CC   useful for suppressing a symptom of an allergic reaction in a subject,
CC   maintaining suppression of a Th2 immune response and maintaining
CC   stimulation of a Th1 immune response. One method is useful in preventing
CC   the onset of, or rapidly suppress, antigen-stimulated inflammation in a
CC   host. The immunostimulatory nucleic acids are useful in the treatment and
CC   prevention of inflammation associated with allergy, including antigen-
CC   stimulated granulocyte infiltration of tissue, such as occurs in the
CC   respiratory passages of asthmatics during an asthma attack, for boosting
CC   the immune responsiveness of a mammalian host to a sensitizing antigen,
CC   and for treating a host suffering from inflammatory conditions such as
CC   asthma, nasal polyposis, allergic rhinitis, atopic dermatitis, allergic
CC   conjunctivitis, eosinophilic fasciitis, idiopathic hypereosinophilic
CC   syndrome, and cutaneous basophil hypersensitivity. The present sequence
CC   represents the nucleotide sequence of an immunomodulatory oligonucleotide
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 37
AAS16348
ID   AAS16348 standard; DNA; 22 BP.
XX
AC   AAS16348;
XX
DT   14-FEB-2002  (first entry)
XX
DE   ISS polynucleotide #1 useful for treating papillomavirus infections.
XX
KW   Animal papillomavirus infection; human papillomavirus; HPV; STD; wart;
KW   sexually transmitted disease; cervical cancer; immune response;
KW   immunostimulatory sequence; ISS; virucide; phosphorothioate; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .22
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Optionally phosphorothioate linkages"
XX
PN   WO200168117-A2.
XX
PD   20-SEP-2001.
XX
PF   12-MAR-2001; 2001WO-US007842.
XX
PR   10-MAR-2000; 2000US-0188265P.
PR   09-MAR-2001; 2001US-00802445.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Van Nest G;
XX
DR   WPI; 2002-041172/05.
XX
PT   Treating, preventing or ameliorating papillomavirus infections, comprises
PT   administering a composition comprising a polynucleotide having an
PT   immunostimulatory sequence to the individual.
XX
PS   Claim 4; Page 39; 44pp; English.
XX
CC   The present invention relates to novel methods of treating, preventing,
CC   or reducing the severity or recurrence of a symptom of papillomavirus
CC   infection in an individual that has been exposed to or who is infected
CC   with papillomavirus. The method comprises administering a polynucleotide
CC   having an immunostimulatory sequence (ISS; AAS16348-AAS16355) which
CC   induces an immune response. A composition containing ISS is administered
CC   without a papillomavirus antigen. The composition can be included in a
CC   kit for ameliorating or preventing a symptom of human or animal
CC   papillomavirus infection. Infections with human papillomavirus (HPV)
CC   which can be prevented or treated using the method of the invention
CC   include sexually transmitted diseases (STDs), warts, papillomas and
CC   cervical cancer. The present sequence represents one of the ISS
CC   polynucleotides of the invention. Note: The present sequence is shown as
CC   single stranded in the specification, but the patentees state on page 20
CC   that this sequence may be double stranded
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 38
AAL44504
```

```
ID   AAL44504 standard; DNA; 22 BP.
XX
AC   AAL44504;
XX
DT   08-NOV-2002  (first entry)
XX
DE   CpG motif oligonucleotide #12.
XX
KW   Vaccine; immune response; microparticle; ds; adsorbent surface;
KW   poly(alpha-hydroxy acid); polyhydroxy butyric acid; polycaprolactone;
KW   polyorthoester; polycyanoacrylate; detergent; submicron emulsion;
KW   viral infection; bacterial infection; parasitic infection;
KW   CpG oligonucleotide.
XX
OS   Unidentified.
XX
PN   WO200226209-A2.
XX
PD   04-APR-2002.
XX
PF   28-SEP-2001; 2001WO-US030540.
XX
PR   28-SEP-2000; 2000US-0236105P.
PR   30-AUG-2001; 2001US-0315905P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   O'hagan D,  Otten G,  Donnelly JJ,  Polo JM,  Barnett S,  Singh M;
PI   Ulmer J,  Dubensky TW;
XX
DR   WPI; 2002-519084/55.
XX
PT   A microparticle to which a biologically active macromolecule is adsorbed,
PT   for use as a vaccine composition to treat viral, bacterial or parasitic
PT   infections, comprises a polymer microparticle, a detergent and a
PT   submicron emulsion.
XX
PS   Disclosure; Page 46; 100pp; English.
XX
CC   The invention relates to a method of raising an immune response in a host
CC   animal. The method of the invention comprises administering a
CC   microparticle that has an adsorbent surface to which a first biologically
CC   active macromolecule (e.g. a nucleic acid) has been adsorbed. The
CC   microparticle comprises a polymer microparticle of poly(alpha-hydroxy
CC   acid), a polyhydroxy butyric acid, a polycaprolactone, a polyorthoester,
CC   a polycyanoacrylate, a detergent, and submicron emulsion. The method/
CC   microparticle of the invention is useful for immunising a host animal
CC   against viral, bacterial or parasitic infections. The present DNA
CC   sequence represents a CpG oligonucleotide of the invention
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 39
ABA03856
ID   ABA03856 standard; DNA; 22 BP.
XX
AC   ABA03856;
XX
DT   12-FEB-2002  (first entry)
XX
DE   Immunostimulatory sequence (ISS) SEQ ID NO:1.
XX
KW   Immunostimulatory sequence; ISS; immunomodulation; HBV; HCV; infection;
KW   hepatitis B virus; hepatitis C virus; virucide; anti-inflammatory;
KW   hepatotropic; gene therapy; hepatitis infection; viraemia; jaundice;
KW   fatigue; abdominal pain; portal hypertension; cirrhosis;
KW   phosphorothioate; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .22
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
XX
PN   WO200168078-A2.
XX
PD   20-SEP-2001.
XX
PF   12-MAR-2001; 2001WO-US007931.
XX
PR   10-MAR-2000; 2000US-0188301P.
PR   09-MAR-2001; 2001US-00802370.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Van Nest G;
XX
DR   WPI; 2002-049000/06.
XX
PT   Reducing viremia and blood levels of hepatitis virus antigen in an
PT   individual infected with hepatitis B virus, comprises administering a
PT   composition comprising a polynucleotide having an immunostimulatory
PT   sequence.
XX
PS   Claim 5; Page 38; 43pp; English.
XX
CC   The present invention describes a method for reducing viraemia or blood
CC   levels of a hepatitis virus antigen in an individual infected with
CC   hepatitis B virus (HBV). The method comprises administering a composition
CC   comprising a polynucleotide having an immunostimulatory sequence (ISS) to
CC   the individual, where the ISS comprises the sequence 5'-C, G-3', an HBV
CC   antigen is not administered in conjunction with administration of the
CC   composition, and where the composition is administered in an amount
CC   sufficient to reduce HBV viraemia or blood levels of a hepatitis virus
CC   antigen. ISS has virucide, anti-inflammatory and hepatotropic activities,
CC   and can be used in gene therapy. The method can be used for suppressing
CC   and/or ameliorating hepatitis infection in an individual, especially for
CC   preventing, palliating, ameliorating, reducing and/or eliminating one or
CC   more symptoms of HBV or HCV (hepatitis C virus) infection without
CC   administering HBV or HCV antigens. The method is specifically useful for
CC   reducing viraemia and hepatitis viral antigen in blood. ISS-containing
CC   polynucleotides may also be used to improve physical symptoms such as
CC   jaundice, fatigue, abdominal pain, and other clinical/ laboratory
CC   findings associated with hepatitis such as blood levels of liver enzymes,
CC   portal hypertension, or cirrhosis. The present sequence represents a
CC   specifically claimed ISS oligonucleotide for use in the method of the
CC   invention
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.17;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 40
AAL51531
ID   AAL51531 standard; DNA; 22 BP.
XX
AC   AAL51531;
XX
```

DT 10-APR-2003 (first entry)
XX
DE CTL recognition antigen-related oligonucleotide, SEQ ID No 5.
XX
KW Cytotoxic T-lymphocyte recognition antigen; CTL recognition antigen;
KW human T-lymphotrophic leukaemia virus-1; HTLV-1; tumour; health food;
KW immune response-inducible vaccine; ds; primer; probe.
XX
OS Unidentified.
XX
PN WO200290981-A1.
XX
PD 14-NOV-2002.
XX
PF 02-MAY-2002; 2002WO-JP004406.
XX
PR 08-MAY-2001; 2001JP-00137526.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Hanabuchi S, Ohashi T, Kannagi M;
XX
DR WPI; 2003-140232/13.
XX
PT Screening of cytotoxic T-lymphocyte-recognition antigen with a human T-
PT lymphotrophic leukemia virus-1 (HTLV-1) antitumor effect, for use as a
PT vaccine, comprises administering a test substance to a HTLV-1-associated
PT disease animal model.
XX
PS Example 10; Page 29; 53pp; Japanese.
XX
CC The invention comprises a method for screening a cytotoxic T-lymphocyte
CC (CTL) recognition antigen, which includes CTLs with antitumour effect
CC against human T-lymphotrophic leukaemia virus-1 (HTLV-1) tumours. The CTL
CC -recognition antigens identified by the method of the invention are
CC useful as immune response-inducible vaccines, and as components of drug
CC preparations and health foods. The present DNA sequence represents an
CC oligonucleotide that was used in an example of the invention
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

Search completed: April 24, 2004, 15:23:00
Job time : 322 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 15:05:43 ; Search time 64.5333 Seconds
(without alignments)
189.188 Million cell updates/sec

Title: US-09-802-445-1
Perfect score: 22
Sequence: 1 tgactgtgaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	22	100.0	22	4	US-09-235-742-19	Sequence 19, Appl
	2	22	100.0	22	4	US-09-347-343-32	Sequence 32, Appl
	3	22	100.0	22	4	US-09-820-484-1	Sequence 1, Appli
	4	22	100.0	22	4	US-09-820-484-3	Sequence 3, Appli
	5	22	100.0	22	4	US-09-774-403A-1	Sequence 1, Appli
	6	22	100.0	22	4	US-09-296-477-2	Sequence 2, Appli
	7	22	100.0	22	4	US-09-308-036A-1	Sequence 1, Appli
	8	22	100.0	22	4	US-09-791-500-1	Sequence 1, Appli
	9	21	95.5	22	4	US-09-296-477-15	Sequence 15, Appl
	10	20.4	92.7	22	3	US-09-092-314-2	Sequence 2, Appli
	11	20.4	92.7	22	4	US-09-820-484-2	Sequence 2, Appli
	12	20.4	92.7	22	4	US-09-820-484-6	Sequence 6, Appli
	13	20.4	92.7	22	4	US-09-774-403A-2	Sequence 2, Appli
	14	20.4	92.7	22	4	US-09-296-477-1	Sequence 1, Appli
c	15	20.4	92.7	22	4	US-09-296-477-5	Sequence 5, Appli
	16	20.4	92.7	22	4	US-09-296-477-6	Sequence 6, Appli
	17	20.4	92.7	22	4	US-09-791-500-4	Sequence 4, Appli
	18	20.4	92.7	22	4	US-09-791-500-5	Sequence 5, Appli
	19	20.4	92.7	22	4	US-09-791-500-6	Sequence 6, Appli
	20	20	90.9	22	4	US-09-296-477-16	Sequence 16, Appl
	21	19.4	88.2	22	4	US-09-296-477-12	Sequence 12, Appl
	22	18.8	85.5	22	3	US-09-092-314-1	Sequence 1, Appli
	23	18.8	85.5	22	3	US-09-092-314-3	Sequence 3, Appli
	24	18.8	85.5	22	3	US-09-092-314-10	Sequence 10, Appl
	25	18.8	85.5	22	4	US-09-235-742-20	Sequence 20, Appl
	26	18.8	85.5	22	4	US-09-347-343-33	Sequence 33, Appl
	27	18.8	85.5	22	4	US-09-820-484-7	Sequence 7, Appli
	28	18.8	85.5	22	4	US-09-774-403A-3	Sequence 3, Appli
	29	18.8	85.5	22	4	US-09-296-477-3	Sequence 3, Appli
	30	18.8	85.5	22	4	US-09-296-477-8	Sequence 8, Appli
	31	18.8	85.5	22	4	US-09-308-036A-2	Sequence 2, Appli
	32	18.8	85.5	22	4	US-09-791-500-3	Sequence 3, Appli
	33	18.8	85.5	22	4	US-09-791-500-8	Sequence 8, Appli
	34	17.2	78.2	22	3	US-09-092-314-4	Sequence 4, Appli
	35	17.2	78.2	22	4	US-09-296-477-9	Sequence 9, Appli
	36	17.2	78.2	22	4	US-09-296-477-13	Sequence 13, Appl
	37	17.2	78.2	22	4	US-09-791-500-9	Sequence 9, Appli
	38	15.6	70.9	22	3	US-09-092-314-5	Sequence 5, Appli
	39	15.6	70.9	22	3	US-09-092-314-7	Sequence 7, Appli
	40	15.6	70.9	22	3	US-09-092-314-8	Sequence 8, Appli
	41	15.6	70.9	22	4	US-09-791-500-2	Sequence 2, Appli
c	42	15.6	70.9	768	4	US-09-543-681A-2526	Sequence 2526, Ap
	43	15.6	70.9	1418	1	US-08-391-615-7	Sequence 7, Appli
	44	15.6	70.9	1830	3	US-09-019-931-2	Sequence 2, Appli
c	45	15.6	70.9	2154	4	US-09-107-532A-2696	Sequence 2696, Ap

ALIGNMENTS

RESULT 1
US-09-235-742-19
; Sequence 19, Application US/09235742
; Patent No. 6498148
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Immunization-Free Methods for Treating
; TITLE OF INVENTION: Antigen-Stimulated Inflammation in a Mammalian Host and
; TITLE OF INVENTION: Shifting the Host's Antigen Immune Responsiveness to a TH1
; TITLE OF INVENTION: Phenotype
; FILE REFERENCE: 6510-170CON4
; CURRENT APPLICATION NUMBER: US/09/235,742
; CURRENT FILING DATE: 1999-01-21
; EARLIER APPLICATION NUMBER: 08/927,120
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 08/593,554
; EARLIER FILING DATE: 1996-01-30
; EARLIER APPLICATION NUMBER: 08/725,968
; EARLIER FILING DATE: 1996-10-04
; EARLIER APPLICATION NUMBER: 60/028,118
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant or Synthetic Sequence
US-09-235-742-19

Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 2
US-09-347-343-32
; Sequence 32, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A

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;  CURRENT FILING DATE: 1999-07-02
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: synthetic oligonucleotide
US-09-347-343-32

  Query Match             100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 3
US-09-820-484-1
; Sequence 1, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
;   NAME/KEY: modified_base
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: disulfide thymine
US-09-820-484-1

  Query Match             100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 4
US-09-820-484-3
; Sequence 3, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: phosphorothioate ISS-ODN
US-09-820-484-3

  Query Match             100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 5
US-09-774-403A-1
; Sequence 1, Application US/09774403A
; Patent No. 6552006
; GENERAL INFORMATION:
;  APPLICANT: Eyal Raz
;  APPLICANT:  Richard Kornbluth
;  APPLICANT:  Antonio Catanzaro
;  APPLICANT:  Tomoko Hayashi
;  APPLICANT:  Dennis Carson
;  TITLE OF INVENTION: Immunomodulatory Polynucleotides in
;  TITLE OF INVENTION:  Treatment of Infection by an Intracellular Pathogen
;  FILE REFERENCE: UCAL166
;  CURRENT APPLICATION NUMBER: US/09/774,403A
;  CURRENT FILING DATE:  2002-04-15
;  PRIOR APPLICATION NUMBER: 60/179,353
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Immunomodulatory sequence
US-09-774-403A-1

  Query Match             100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 6
US-09-296-477-2
; Sequence 2, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
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```
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-296-477-2

  Query Match             100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 7
US-09-308-036A-1
; Sequence 1, Application US/09308036A
; Patent No. 6610661
; GENERAL INFORMATION:
;  APPLICANT: Carson, Dennis A.
;  APPLICANT:  Raz, Eyal
;  APPLICANT:  Roman, Mark
;  TITLE OF INVENTION: Immunostimulatory
;  TITLE OF INVENTION:  Polynucleotide/Immunomodulatory Molecule Conjugates
;  FILE REFERENCE: 6510-172CIP
;  CURRENT APPLICATION NUMBER: US/09/308,036A
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: PCT/US97/19004
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: 60/028,118
;  PRIOR FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DY1018 polynucleotide
US-09-308-036A-1

  Query Match             100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 8
US-09-791-500-1
; Sequence 1, Application US/09791500
; Patent No. 6613751
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Rachmilewitz, Daniel
;  TITLE OF INVENTION: Method for Treating Inflammatory Bowel
;  TITLE OF INVENTION:  Disease and Other Forms of Gastrointestinal Inflammation.
;  FILE REFERENCE: 6510-202US1
;  CURRENT APPLICATION NUMBER: US/09/791,500
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-1

  Query Match             100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 9
US-09-296-477-15
; Sequence 15, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (11)...(11)
;   OTHER INFORMATION: 5-bromocytosine
US-09-296-477-15

  Query Match             95.5%;  Score 21;  DB 4;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.065;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| ||||||||||
Db          1 TGACTGTGAANGTTCGAGATGA 22


RESULT 10
US-09-092-314-2
; Sequence 2, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
;  APPLICANT:  Raz, Eyal
;  APPLICANT:  Roman, Mark
;  TITLE OF INVENTION:  Inhibitors of DNA Immunostimulatory
;  TITLE OF INVENTION:  Sequence Activity
; Patent No. 6225292
```

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;  FILE REFERENCE:  6510-173US1
;  CURRENT APPLICATION NUMBER: US/09/092,314
;  CURRENT FILING DATE:  1998-06-05
;  PRIOR APPLICATION NUMBER:  60/048,794
;  PRIOR FILING DATE:  1997-06-06
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

  Query Match             92.7%;  Score 20.4;  DB 3;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.13;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||||||| |||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 11
US-09-820-484-2
; Sequence 2, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mutated ODN
;   NAME/KEY: modified_base
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: disulfide thymine
US-09-820-484-2

  Query Match             92.7%;  Score 20.4;  DB 4;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.13;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| ||||||||||
Db          1 TGACTGTGAACCTTCGAGATGA 22


RESULT 12
US-09-820-484-6
; Sequence 6, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mutated control ODN
US-09-820-484-6

  Query Match             92.7%;  Score 20.4;  DB 4;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.13;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| ||||||||||
Db          1 TGACTGTGAACCTTCGAGATGA 22


RESULT 13
US-09-774-403A-2
; Sequence 2, Application US/09774403A
; Patent No. 6552006
; GENERAL INFORMATION:
;  APPLICANT: Eyal Raz
;  APPLICANT:  Richard Kornbluth
;  APPLICANT:  Antonio Catanzaro
;  APPLICANT:  Tomoko Hayashi
;  APPLICANT:  Dennis Carson
;  TITLE OF INVENTION: Immunomodulatory Polynucleotides in
;  TITLE OF INVENTION:  Treatment of Infection by an Intracellular Pathogen
;  FILE REFERENCE: UCAL166
;  CURRENT APPLICATION NUMBER: US/09/774,403A
;  CURRENT FILING DATE:  2002-04-15
;  PRIOR APPLICATION NUMBER: 60/179,353
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Control sequence
US-09-774-403A-2

  Query Match             92.7%;  Score 20.4;  DB 4;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.13;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| ||||||||||
Db          1 TGACTGTGAAGGTTCGAGATGA 22


RESULT 14
US-09-296-477-1
; Sequence 1, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
```

```
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-296-477-1

  Query Match             92.7%;  Score 20.4;  DB 4;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.13;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||| ||||||||||||||||||
Db          1 TGACCGTGAACGTTCGAGATGA 22


RESULT 15
US-09-296-477-5/c
; Sequence 5, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-296-477-5

  Query Match             92.7%;  Score 20.4;  DB 4;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.13;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||| ||||||||||||||||||
Db         22 TGACCGTGAACGTTCGAGATGA 1


RESULT 16
US-09-296-477-6
; Sequence 6, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-296-477-6

  Query Match             92.7%;  Score 20.4;  DB 4;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.13;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||||||| ||||||
Db          1 TGACTGTGAACGTTCCAGATGA 22


RESULT 17
US-09-791-500-4
; Sequence 4, Application US/09791500
; Patent No. 6613751
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Rachmilewitz, Daniel
;  TITLE OF INVENTION: Method for Treating Inflammatory Bowel
;  TITLE OF INVENTION:  Disease and Other Forms of Gastrointestinal Inflammation.
;  FILE REFERENCE: 6510-202US1
;  CURRENT APPLICATION NUMBER: US/09/791,500
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-4

  Query Match             92.7%;  Score 20.4;  DB 4;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.13;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| ||||||||||
Db          1 TGACTGTGAAGGTTCGAGATGA 22


RESULT 18
US-09-791-500-5
; Sequence 5, Application US/09791500
; Patent No. 6613751
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
```

; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202US1
; CURRENT APPLICATION NUMBER: US/09/791,500
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-5

Query Match 92.7%; Score 20.4; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.13;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||| |||||||
Db 1 TGACTGTGAACGTTAGAGATGA 22

RESULT 19
US-09-791-500-6
; Sequence 6, Application US/09791500
; Patent No. 6613751
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202US1
; CURRENT APPLICATION NUMBER: US/09/791,500
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-6

Query Match 92.7%; Score 20.4; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.13;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||| |||||||
Db 1 TGACTGTGAACGTTAGAGATGA 22

RESULT 20
US-09-296-477-16
; Sequence 16, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)...(11)
; OTHER INFORMATION: 5-bromocytosine
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (15)...(15)
; OTHER INFORMATION: 5-bromocytosine
US-09-296-477-16

Query Match 90.9%; Score 20; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
|||||||||| ||| |||||||
Db 1 TGACTGTGAANGTTNGAGATGA 22

RESULT 21
US-09-296-477-12
; Sequence 12, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)...(11)
; OTHER INFORMATION: 5-bromocytosine
US-09-296-477-12

Query Match 88.2%; Score 19.4; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.43;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
|||||||||| |||| ||||||
Db 1 TGACTGTGAANGTTCCAGATGA 22

RESULT 22
US-09-092-314-1

; Sequence 1, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-1

Query Match 85.5%; Score 18.8; DB 3; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.87;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| ||| |||||||
Db 1 TGACTGTGAAGGTTAGAGATGA 22

RESULT 23
US-09-092-314-3
; Sequence 3, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-3

Query Match 85.5%; Score 18.8; DB 3; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.87;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| || |||||||
Db 1 TGACTGTGAACCTTAGAGATGA 22

RESULT 24
US-09-092-314-10
; Sequence 10, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-10

Query Match 85.5%; Score 18.8; DB 3; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.87;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| ||| |||||||
Db 1 TGACTGTGAATGTTAGAGATGA 22

RESULT 25
US-09-235-742-20
; Sequence 20, Application US/09235742
; Patent No. 6498148
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Immunization-Free Methods for Treating
; TITLE OF INVENTION: Antigen-Stimulated Inflammation in a Mammalian Host and
; TITLE OF INVENTION: Shifting the Host's Antigen Immune Responsiveness to a TH1
; TITLE OF INVENTION: Phenotype
; FILE REFERENCE: 6510-170CON4
; CURRENT APPLICATION NUMBER: US/09/235,742
; CURRENT FILING DATE: 1999-01-21
; EARLIER APPLICATION NUMBER: 08/927,120
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 08/593,554
; EARLIER FILING DATE: 1996-01-30
; EARLIER APPLICATION NUMBER: 08/725,968
; EARLIER FILING DATE: 1996-10-04
; EARLIER APPLICATION NUMBER: 60/028,118
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant or Synthetic Sequence
US-09-235-742-20

Query Match 85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.87;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| ||| |||||||
Db 1 TGACTGTGAAGGTTGGAGATGA 22

RESULT 26
US-09-347-343-33
; Sequence 33, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.

; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 22
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-33

Query Match 85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.87;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| || |||||||
Db 1 TGACTGTGAACCTTAGAGATGA 22

RESULT 27
US-09-820-484-7
; Sequence 7, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188US1
; CURRENT APPLICATION NUMBER: US/09/820,484
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mODN
US-09-820-484-7

Query Match 85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.87;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| || |||||||
Db 1 TGACTGTGAACCTTAGAGATGA 22

RESULT 28
US-09-774-403A-3
; Sequence 3, Application US/09774403A
; Patent No. 6552006
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen
; FILE REFERENCE: UCAL166
; CURRENT APPLICATION NUMBER: US/09/774,403A
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control sequence
US-09-774-403A-3

Query Match 85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.87;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| ||| |||||||
Db 1 TGACTGTGAAGGTTAGAGATGA 22

RESULT 29
US-09-296-477-3
; Sequence 3, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-296-477-3

Query Match 85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.87;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| ||| |||||||
Db 1 TGACTGTGAAGGTTAGAGATGA 22

RESULT 30
US-09-296-477-8
; Sequence 8, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE

```
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-296-477-8

  Query Match             85.5%;  Score 18.8;  DB 4;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 0.87;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||| | |||||
Db          1 TGACTGTGAACGTTAGCGATGA 22


RESULT 31
US-09-308-036A-2
; Sequence 2, Application US/09308036A
; Patent No. 6610661
; GENERAL INFORMATION:
;  APPLICANT: Carson, Dennis A.
;  APPLICANT:  Raz, Eyal
;  APPLICANT:  Roman, Mark
;  TITLE OF INVENTION: Immunostimulatory
;  TITLE OF INVENTION:  Polynucleotide/Immunomodulatory Molecule Conjugates
;  FILE REFERENCE: 6510-172CIP
;  CURRENT APPLICATION NUMBER: US/09/308,036A
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: PCT/US97/19004
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: 60/028,118
;  PRIOR FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: D41019 polynucleotide
US-09-308-036A-2

  Query Match             85.5%;  Score 18.8;  DB 4;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 0.87;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| ||| |||||||
Db          1 TGACTGTGAAGGTTGGAGATGA 22


RESULT 32
US-09-791-500-3
; Sequence 3, Application US/09791500
; Patent No. 6613751
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Rachmilewitz, Daniel
;  TITLE OF INVENTION: Method for Treating Inflammatory Bowel
;  TITLE OF INVENTION:  Disease and Other Forms of Gastrointestinal Inflammation.
;  FILE REFERENCE: 6510-202US1
;  CURRENT APPLICATION NUMBER: US/09/791,500
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-3

  Query Match             85.5%;  Score 18.8;  DB 4;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 0.87;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||||  || |||||||
Db          1 TGACTGTGAACCTTAGAGATGA 22


RESULT 33
US-09-791-500-8
; Sequence 8, Application US/09791500
; Patent No. 6613751
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Rachmilewitz, Daniel
;  TITLE OF INVENTION: Method for Treating Inflammatory Bowel
;  TITLE OF INVENTION:  Disease and Other Forms of Gastrointestinal Inflammation.
;  FILE REFERENCE: 6510-202US1
;  CURRENT APPLICATION NUMBER: US/09/791,500
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-8

  Query Match             85.5%;  Score 18.8;  DB 4;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 0.87;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| ||| |||||||
Db          1 TGACTGTGAATGTTAGAGATGA 22


RESULT 34
US-09-092-314-4
; Sequence 4, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
;  APPLICANT:  Raz, Eyal
;  APPLICANT:  Roman, Mark
;  TITLE OF INVENTION:  Inhibitors of DNA Immunostimulatory
;  TITLE OF INVENTION:  Sequence Activity
; Patent No. 6225292
;  FILE REFERENCE:  6510-173US1
;  CURRENT APPLICATION NUMBER: US/09/092,314
;  CURRENT FILING DATE:  1998-06-05
;  PRIOR APPLICATION NUMBER:  60/048,794
;  PRIOR FILING DATE:  1997-06-06
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

  Query Match             78.2%;  Score 17.2;  DB 3;  Length 22;
  Best Local Similarity   86.4%;  Pred. No. 5.8;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||  || |||||||
Db          1 TGACTGTGAAGCTTAGAGATGA 22


RESULT 35
US-09-296-477-9
; Sequence 9, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-296-477-9

  Query Match             78.2%;  Score 17.2;  DB 4;  Length 22;
  Best Local Similarity   86.4%;  Pred. No. 5.8;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||||||| ||  |||
Db          1 TGACTGTGAACGTTAGACGTGA 22


RESULT 36
US-09-296-477-13
; Sequence 13, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-296-477-13

  Query Match             78.2%;  Score 17.2;  DB 4;  Length 22;
  Best Local Similarity   86.4%;  Pred. No. 5.8;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||  || |||||||
Db          1 TGACTGTGAAGCTTAGAGATGA 22


RESULT 37
US-09-791-500-9
; Sequence 9, Application US/09791500
; Patent No. 6613751
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Rachmilewitz, Daniel
;  TITLE OF INVENTION: Method for Treating Inflammatory Bowel
;  TITLE OF INVENTION:  Disease and Other Forms of Gastrointestinal Inflammation.
;  FILE REFERENCE: 6510-202US1
;  CURRENT APPLICATION NUMBER: US/09/791,500
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-9

  Query Match             78.2%;  Score 17.2;  DB 4;  Length 22;
  Best Local Similarity   86.4%;  Pred. No. 5.8;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||  |||| |||||||
Db          1 TGACTGTGGTCGTTAGAGATGA 22


RESULT 38
US-09-092-314-5
; Sequence 5, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
;  APPLICANT:  Raz, Eyal
;  APPLICANT:  Roman, Mark
;  TITLE OF INVENTION:  Inhibitors of DNA Immunostimulatory
;  TITLE OF INVENTION:  Sequence Activity
; Patent No. 6225292
;  FILE REFERENCE:  6510-173US1
;  CURRENT APPLICATION NUMBER: US/09/092,314
;  CURRENT FILING DATE:  1998-06-05
;  PRIOR APPLICATION NUMBER:  60/048,794
;  PRIOR FILING DATE:  1997-06-06
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-09-092-314-5

  Query Match             70.9%;  Score 15.6;  DB 3;  Length 22;
```

Best Local Similarity 81.8%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||  | ||  |||||||
Db          1 TGACTGTGTTCCTTAGAGATGA 22
```

RESULT 39
US-09-092-314-7
; Sequence 7, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-7

Query Match 70.9%; Score 15.6; DB 3; Length 22;
Best Local Similarity 81.8%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||  | ||  |||||||
Db          1 TGACTGTGGAGGTCAGAGATGA 22
```

RESULT 40
US-09-092-314-8
; Sequence 8, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-8

Query Match 70.9%; Score 15.6; DB 3; Length 22;
Best Local Similarity 81.8%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||  | | |||||||
Db          1 TGACTGTGAGGGCTAGAGATGA 22
```

Search completed: April 24, 2004, 17:02:45
Job time : 65.5333 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 15:59:19 ; Search time 295.533 Seconds
(without alignments)
335.630 Million cell updates/sec

Title: US-09-802-445-1
Perfect score: 22
Sequence: 1 tgactgtgaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Maximum Match 100%
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	22	9	US-09-802-686-1	Sequence 1, Appli
2	22	100.0	22	9	US-09-802-685-1	Sequence 1, Appli
3	22	100.0	22	9	US-09-791-500-1	Sequence 1, Appli
4	22	100.0	22	9	US-09-802-376-1	Sequence 1, Appli
5	22	100.0	22	9	US-09-802-370-1	Sequence 1, Appli
6	22	100.0	22	9	US-09-802-445-1	Sequence 1, Appli
7	22	100.0	22	9	US-09-820-484-1	Sequence 1, Appli
8	22	100.0	22	9	US-09-820-484-3	Sequence 3, Appli
9	22	100.0	22	9	US-09-828-505-1	Sequence 1, Appli
10	22	100.0	22	9	US-09-967-881-2	Sequence 2, Appli
11	22	100.0	22	10	US-09-927-422A-1	Sequence 1, Appli
12	22	100.0	22	10	US-09-738-046A-3	Sequence 3, Appli
13	22	100.0	22	10	US-09-927-884-1	Sequence 1, Appli
14	22	100.0	22	10	US-09-802-359-1	Sequence 1, Appli
15	22	100.0	22	10	US-09-967-464-19	Sequence 19, Appl
16	22	100.0	22	10	US-09-848-986-1	Sequence 1, Appli
17	22	100.0	22	13	US-10-214-288-1	Sequence 1, Appli
18	22	100.0	22	13	US-10-328-578-2	Sequence 2, Appli
19	22	100.0	22	13	US-10-328-578-24	Sequence 24, Appl
20	22	100.0	22	13	US-10-328-578-79	Sequence 79, Appl
21	22	100.0	22	13	US-10-353-917-1	Sequence 1, Appli
22	22	100.0	22	15	US-10-056-420-4	Sequence 4, Appli
23	22	100.0	22	15	US-10-033-243-2	Sequence 2, Appli
24	22	100.0	22	15	US-10-033-243-40	Sequence 40, Appl
25	22	100.0	22	15	US-10-033-243-59	Sequence 59, Appl
26	22	100.0	22	15	US-10-099-512-1	Sequence 1, Appli
27	22	100.0	22	15	US-10-229-208-19	Sequence 19, Appl
28	22	100.0	22	15	US-10-253-117-32	Sequence 32, Appl
29	22	100.0	22	15	US-10-233-121A-1	Sequence 1, Appli
30	22	100.0	22	15	US-10-219-143-1	Sequence 1, Appli
31	22	100.0	22	15	US-10-214-799-2	Sequence 2, Appli
32	22	100.0	22	15	US-10-340-275-1	Sequence 1, Appli
33	22	100.0	22	15	US-10-340-275-3	Sequence 3, Appli
34	22	100.0	22	15	US-10-339-885-1	Sequence 1, Appli
35	22	100.0	22	15	US-10-339-885-3	Sequence 3, Appli
36	22	100.0	22	15	US-10-176-883-2	Sequence 2, Appli
37	22	100.0	22	15	US-10-176-883-24	Sequence 24, Appl
38	22	100.0	22	15	US-10-176-883-79	Sequence 79, Appl
39	22	100.0	22	15	US-10-176-883-134	Sequence 134, App
40	22	100.0	22	15	US-10-412-151-1	Sequence 1, Appli
41	22	100.0	22	15	US-10-177-826-2	Sequence 2, Appli
42	22	100.0	22	15	US-10-177-826-24	Sequence 24, Appl
43	22	100.0	22	15	US-10-177-826-79	Sequence 79, Appl
44	22	100.0	22	15	US-10-177-826-134	Sequence 134, App
45	22	100.0	22	16	US-10-357-760-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-802-686-1
; Sequence 1, Application US/09802686
; Patent No. US20010046967A1
; GENERAL INFORMATION:
; APPLICANT: Dynavax Technologies Corporation
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING
; TITLE OF INVENTION: RESPIRATORY VIRAL INFECTION USING IMMUNOMODULATORY
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES
; FILE REFERENCE: 377882000900
; CURRENT APPLICATION NUMBER: US/09/802,686
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,583
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-686-1

Query Match 100.0%; Score 22; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 2
US-09-802-685-1
; Sequence 1, Application US/09802685

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; Patent No. US20020028784A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Eiden, Joseph J., Jr.
;  TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING VIRAL
;  TITLE OF INVENTION:  INFECTIONS USING IMMUNOMODULATORY POLYNUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 377882001600
;  CURRENT APPLICATION NUMBER: US/09/802,685
;  CURRENT FILING DATE:  2001-03-09
;  PRIOR APPLICATION NUMBER: U.S. 60/188,302
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-685-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 3
US-09-791-500-1
; Sequence 1, Application US/09791500
; Patent No. US20020042387A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Rachmilewitz, Daniel
;  TITLE OF INVENTION: Method for Treating Inflammatory Bowel
;  TITLE OF INVENTION:  Disease and Other Forms of Gastrointestinal Inflammation.
;  FILE REFERENCE: 6510-202US1
;  CURRENT APPLICATION NUMBER: US/09/791,500
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 4
US-09-802-376-1
; Sequence 1, Application US/09802376
; Patent No. US20020055477A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
;  FILE REFERENCE: 377882001700
;  CURRENT APPLICATION NUMBER: US/09/802,376
;  CURRENT FILING DATE:  2001-03-09
;  PRIOR APPLICATION NUMBER: 60/188,557
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 5
US-09-802-370-1
; Sequence 1, Application US/09802370
; Patent No. US20020098199A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Eiden, Joseph J. Jr.
;  TITLE OF INVENTION: METHODS OF SUPPRESSING HEPATITIS VIRUS
;  TITLE OF INVENTION:  INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 377882001200
;  CURRENT APPLICATION NUMBER: US/09/802,370
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: 60/188,301
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-370-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 6
US-09-802-445-1
; Sequence 1, Application US/09802445
; Patent No. US20020107212A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Eiden, Joseph J. Jr.
;  TITLE OF INVENTION: METHODS OF REDUCING PAPILLOMAVIRUS INFECTION USING IMMUNOMODULA'
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 377882001300
;  CURRENT APPLICATION NUMBER: US/09/802,445
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: 60/188,265
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
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;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-445-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 7
US-09-820-484-1
; Sequence 1, Application US/09820484
; Patent No. US20020142977A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
;   NAME/KEY: modified_base
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: disulfide thymine
US-09-820-484-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 8
US-09-820-484-3
; Sequence 3, Application US/09820484
; Patent No. US20020142977A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: phosphorothioate ISS-ODN
US-09-820-484-3

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 9
US-09-828-505-1
; Sequence 1, Application US/09828505
; Patent No. US20020142978A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Takabayashi, Kenji
;  APPLICANT:  Nguyen, Minh-Duc
;  TITLE OF INVENTION: Synergistic Improvements to
;  TITLE OF INVENTION:  Polynucleotide Vaccines
;  FILE REFERENCE: 6510-203
;  CURRENT APPLICATION NUMBER: US/09/828,505
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: 60/195,890
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Immunomodulatory nucleic acid sequence
US-09-828-505-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 10
US-09-967-881-2
; Sequence 2, Application US/09967881
; Publication No. US20020192184A1
; GENERAL INFORMATION:
;  APPLICANT: Assistance Publique - Hopitaux de Paris
;  APPLICANT:  Institut National de la Sante et de la Recherche M
;  APPLICANT:  Carpentier, Antoine
;  TITLE OF INVENTION: Use of Stabilised Oligonucleotides for Preparing A Medicament wi
;  TITLE OF INVENTION:  Antitumor Activity
;  FILE REFERENCE: 267/246 US
;  CURRENT APPLICATION NUMBER: US/09/967,881
;  CURRENT FILING DATE:  2001-09-28
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
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;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Oligodeoxynucleotide
US-09-967-881-2

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 11
US-09-927-422A-1
; Sequence 1, Application US/09927422A
; Publication No. US20030022852A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  APPLICANT:  Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  TITLE OF INVENTION: BIODEGRADABLE IMMUNOMODULATORY
;  TITLE OF INVENTION:  FORMULATIONS AND METHODS FOR USE THEREOF
;  FILE REFERENCE: 377882001420
;  CURRENT APPLICATION NUMBER: US/09/927,422A
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/802,359
;  PRIOR FILING DATE: 2001-03-09
;  PRIOR APPLICATION NUMBER: U.S. 60/188,30
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-927-422A-1

  Query Match             100.0%;  Score 22;  DB 10;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 12
US-09-738-046A-3
; Sequence 3, Application US/09738046A
; Publication No. US20030054007A1
; GENERAL INFORMATION:
;  APPLICANT: FELGNER, PHILIP L.
;  APPLICANT:  ZELPHATI, OLIVIER
;  TITLE OF INVENTION: INTRACELLULAR PROTEIN DELIVERY
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS OF USE
;  FILE REFERENCE: GTSYS.004A
;  CURRENT APPLICATION NUMBER: US/09/738,046A
;  CURRENT FILING DATE:  2000-12-15
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence containing CpG sequence
US-09-738-046A-3

  Query Match             100.0%;  Score 22;  DB 10;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 13
US-09-927-884-1
; Sequence 1, Application US/09927884
; Publication No. US20030059773A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  APPLICANT:  Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND
;  TITLE OF INVENTION:  METHODS FOR USE THEREOF
;  FILE REFERENCE: 377882001720
;  CURRENT APPLICATION NUMBER: US/09/927,884
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/802,376
;  PRIOR FILING DATE: 2001-03-09
;  PRIOR APPLICATION NUMBER: U.S. 60/188,557
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-927-884-1

  Query Match             100.0%;  Score 22;  DB 10;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 14
US-09-802-359-1
; Sequence 1, Application US/09802359
; Publication No. US20030129251A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
;  FILE REFERENCE: 37788201400
;  CURRENT APPLICATION NUMBER: US/09/802,359
;  CURRENT FILING DATE:  2001-03-09
;  PRIOR APPLICATION NUMBER: 60/188,303
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

  Query Match             100.0%;  Score 22;  DB 10;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 15
US-09-967-464-19
; Sequence 19, Application US/09967464
; Publication No. US20030138453A1
; GENERAL INFORMATION:
;  APPLICANT: O'Hagan, Derek
;  APPLICANT:  Otten, Gillis
;  APPLICANT:  Donnelly, John J.
;  APPLICANT:  Polo, John M.
;  APPLICANT:  Barnett, Susan
;  APPLICANT:  Singh, Mamohan
;  APPLICANT:  Ulmer, Jeffrey
;  APPLICANT:  Dubensky, Jr., Thomas W.
;  TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF HETEROLOGOUS NUCLEIC ACIDS
;  FILE REFERENCE: PP16269.004
;  CURRENT APPLICATION NUMBER: US/09/967,464
;  CURRENT FILING DATE:  2002-04-11
;  PRIOR APPLICATION NUMBER: 60/236,105
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: 60/315,905
;  PRIOR FILING DATE: 2001-08-30
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial sequence is synthesized
US-09-967-464-19

  Query Match             100.0%;  Score 22;  DB 10;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 16
US-09-848-986-1
; Sequence 1, Application US/09848986
; Publication No. US20030176373A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Lois, Augusto F.
;  APPLICANT:  Takabayashi, Kenji
;  TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
;  TITLE OF INVENTION:  Methods of Use Thereof
;  FILE REFERENCE: 06510168US1
;  CURRENT APPLICATION NUMBER: US/09/848,986
;  CURRENT FILING DATE:  2001-05-03
;  PRIOR APPLICATION NUMBER: us 60/262321
;  PRIOR FILING DATE: 2001-01-17
;  PRIOR APPLICATION NUMBER: us 60/202,274
;  PRIOR FILING DATE: 2000-05-05
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: ISS-ODN
US-09-848-986-1

  Query Match             100.0%;  Score 22;  DB 10;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 17
US-10-214-288-1
; Sequence 1, Application US/10214288
; Publication No. US20030064064A1
; GENERAL INFORMATION:
;  APPLICANT: Dino, Dina
;  TITLE OF INVENTION: Methods of Treating IgE-Associated
;  TITLE OF INVENTION:  Disorders and Compositions for Use Therein
;  FILE REFERENCE: 377882000601
;  CURRENT APPLICATION NUMBER: US/10/214,288
;  CURRENT FILING DATE:  2002-08-06
;  PRIOR APPLICATION NUMBER: US 09/397,198
;  PRIOR FILING DATE: 1999-09-16
;  PRIOR APPLICATION NUMBER: US 60/100,838
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/136,600
;  PRIOR FILING DATE: 1999-05-28
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: ISS sequence
US-10-214-288-1

  Query Match             100.0%;  Score 22;  DB 13;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 18
US-10-328-578-2
; Sequence 2, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
```

US-10-328-578-2

Query Match 100.0%; Score 22; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22
```

RESULT 19
US-10-328-578-24
; Sequence 24, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen L.
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen F.
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-III
; FILE REFERENCE: 377882002020
; CURRENT APPLICATION NUMBER: US/10/328,578
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 10/176,883
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/375,253
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 10/177,826
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-328-578-24

Query Match 100.0%; Score 22; DB 13; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.3;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||:||||||||
Db          1 TGACTGTGAACGUTCGAGATGA 22
```

RESULT 20
US-10-328-578-79
; Sequence 79, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen L.
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen F.
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-III
; FILE REFERENCE: 377882002020
; CURRENT APPLICATION NUMBER: US/10/328,578
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 10/176,883
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/375,253
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 10/177,826
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-328-578-79

Query Match 100.0%; Score 22; DB 13; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.3;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||:||||||||
Db          1 TGACTGTGAACGTUCGAGATGA 22
```

RESULT 21
US-10-353-917-1
; Sequence 1, Application US/10353917
; Publication No. US20030212028A1
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen
; FILE REFERENCE: UCAL-166CON
; CURRENT APPLICATION NUMBER: US/10/353,917
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 09/774,403
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory sequence
US-10-353-917-1

Query Match 100.0%; Score 22; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22
```

RESULT 22
US-10-056-420-4
; Sequence 4, Application US/10056420
; Publication No. US20030044428A1
; GENERAL INFORMATION:
; APPLICANT: Moss, Ronald B.
; APPLICANT: Carlo, Dennis J.
; TITLE OF INVENTION: Method For Treating an HIV-Infected
; TITLE OF INVENTION: Individual By Combining Immunization With Structured
; TITLE OF INVENTION: Interruption of Anti-Retroviral Treatment
; FILE REFERENCE: P-IM 5158
; CURRENT APPLICATION NUMBER: US/10/056,420
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/264,476
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0

```
; SEQ ID NO 4
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: exemplary ISS  sequence
US-10-056-420-4

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 23
US-10-033-243-2
; Sequence 2, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-2

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.3;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||||||:|||||||||
Db          1 TGACTGTGAACGTUCGAGATGA 22


RESULT 24
US-10-033-243-40
; Sequence 40, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-40

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.3;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||||||:|||||||||
Db          1 TGACTGTGAACGTUCGAGATGA 22


RESULT 25
US-10-033-243-59
; Sequence 59, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-59

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 26
US-10-099-512-1
; Sequence 1, Application US/10099512
; Publication No. US20030078223A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Broide, David
;  TITLE OF INVENTION: Compositions and Methods for Modulating
;  TITLE OF INVENTION:  an Immune Response
;  FILE REFERENCE: UCAL-170CIP15
;  CURRENT APPLICATION NUMBER: US/10/099,512
;  CURRENT FILING DATE:  2002-03-15
;  PRIOR APPLICATION NUMBER: 09/235,742
;  PRIOR FILING DATE: 1999-01-21
;  PRIOR APPLICATION NUMBER: 08/927,120
;  PRIOR FILING DATE: 1997-09-05
;  PRIOR APPLICATION NUMBER: 09/265,191
;  PRIOR FILING DATE: 1999-03-10
;  PRIOR APPLICATION NUMBER: 08/593,554
;  PRIOR FILING DATE: 1996-01-30
;  PRIOR APPLICATION NUMBER: 60/276,865
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic DNA
```

US-10-099-512-1

Query Match 100.0%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 27
US-10-229-208-19
; Sequence 19, Application US/10229208
; Publication No. US20030092663A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Immunization-Free Methods for Treating
; TITLE OF INVENTION: Antigen-Stimulated Inflammation in a Mammalian Host and
; TITLE OF INVENTION: Shifting the Host's Antigen Immune Responsiveness to a TH1
; TITLE OF INVENTION: Phenotype
; FILE REFERENCE: UCAL-170CON9
; CURRENT APPLICATION NUMBER: US/10/229,208
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: 09/235,742
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 08/927,120
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant or Synthetic Sequence with a
; OTHER INFORMATION: phosphothioate backbone
US-10-229-208-19

Query Match 100.0%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 28
US-10-253-117-32
; Sequence 32, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 22
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-32

Query Match 100.0%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 29
US-10-233-121A-1
; Sequence 1, Application US/10233121A
; Publication No. US20030125284A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, EYAL
; APPLICANT: LOIS, AUGUSTO
; APPLICANT: TAKABAYASHI, KENJI
; TITLE OF INVENTION: AGENTS THAT MODULATE DNA-PK ACTIVITY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: UCAL-168DIV
; CURRENT APPLICATION NUMBER: US/10/233,121A
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 09/848,986
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/202,274
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/262,321
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphodiester or phosphorothioate oligonucleotide
US-10-233-121A-1

Query Match 100.0%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 30
US-10-219-143-1
; Sequence 1, Application US/10219143
; Publication No. US20030130217A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202US1
; CURRENT APPLICATION NUMBER: US/10/219,143
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/791,500
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
US-10-219-143-1

Query Match 100.0%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||

```
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 31
US-10-214-799-2
; Sequence 2, Application US/10214799
; Publication No. US20030133988A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon,Karen L. and Dina,Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY COMPOSITIONS,
;  TITLE OF INVENTION:  FORMULATIONS, AND METHODS OF USE THEREOF
;  FILE REFERENCE: 377882003100
;  CURRENT APPLICATION NUMBER: US/10/214,799
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: US 60/310,743
;  PRIOR FILING DATE: 2001-08-07
;  PRIOR APPLICATION NUMBER: US 60/335,263
;  PRIOR FILING DATE: 2001-10-25
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-214-799-2

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 32
US-10-340-275-1
; Sequence 1, Application US/10340275
; Publication No. US20030143213A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: UCAL-188DIV
;  CURRENT APPLICATION NUMBER: US/10/340,275
;  CURRENT FILING DATE:  2003-01-10
;  PRIOR APPLICATION NUMBER: 09/820,484
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: disulfide thymine
US-10-340-275-1

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 33
US-10-340-275-3
; Sequence 3, Application US/10340275
; Publication No. US20030143213A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: UCAL-188DIV
;  CURRENT APPLICATION NUMBER: US/10/340,275
;  CURRENT FILING DATE:  2003-01-10
;  PRIOR APPLICATION NUMBER: 09/820,484
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: phosphorothioate ISS-ODN
US-10-340-275-3

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 34
US-10-339-885-1
; Sequence 1, Application US/10339885
; Publication No. US20030147870A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: UCAL-188CON
;  CURRENT APPLICATION NUMBER: US/10/339,885
;  CURRENT FILING DATE:  2003-01-10
;  PRIOR APPLICATION NUMBER: 09/820,484
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: disulfide thymine
US-10-339-885-1

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 35
US-10-339-885-3
; Sequence 3, Application US/10339885
; Publication No. US20030147870A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: UCAL-188CON
;  CURRENT APPLICATION NUMBER: US/10/339,885
;  CURRENT FILING DATE:  2003-01-10
;  PRIOR APPLICATION NUMBER: 09/820,484
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: phosphorothioate ISS-ODN
US-10-339-885-3

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 36
US-10-176-883-2
; Sequence 2, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-2

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 37
US-10-176-883-24
; Sequence 24, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-24

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.3;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||||||:||||||||||
Db          1 TGACTGTGAACGUTCGAGATGA 22


RESULT 38
US-10-176-883-79
; Sequence 79, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
```

```
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-79

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 0.3;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||:||||||||
Db          1 TGACTGTGAACGTUCGAGATGA 22


RESULT 39
US-10-176-883-134
; Sequence 134, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 134
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-134

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 40
US-10-412-151-1
; Sequence 1, Application US/10412151
; Publication No. US20030176389A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Rachmilewitz, Daniel
;  TITLE OF INVENTION: Method for Treating Inflammatory Bowel
;  TITLE OF INVENTION:  Disease and Other Forms of Gastrointestinal Inflammation.
;  FILE REFERENCE: UCAL-202CON
;  CURRENT APPLICATION NUMBER: US/10/412,151
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: 09/791,500
;  PRIOR FILING DATE: 2001-02-22
;  PRIOR APPLICATION NUMBER: 60/184,256
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
;   OTHER INFORMATION: oligonucleotide primer
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide primer
US-10-412-151-1

  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


Search completed: April 24, 2004, 18:33:12
Job time : 296.533 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 15:03:13 ; Search time 2700.13 Seconds
(without alignments)
243.309 Million cell updates/sec

Title: US-09-802-445-1
Perfect score: 22
Sequence: 1 tgactgtgaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18.8	85.5	521	28	BH859011	BH859011 S5_182b_t
	2	18.4	83.6	571	12	BM042508	BM042508 603615795
c	3	17.8	80.9	492	29	CE751403	CE751403 tigr-gss-
c	4	17.8	80.9	561	28	AZ755668	AZ755668 ev02g09.x
	5	17.8	80.9	867	28	BZ558601	BZ558601 pa98401_2
	6	17.8	80.9	961	10	BF971856	BF971856 602240444
c	7	17.4	79.1	489	28	AZ060178	AZ060178 RPCI-23-4
c	8	17.4	79.1	530	28	AZ886419	AZ886419 RPCI-23-1
	9	17.2	78.2	374	28	AQ245026	AQ245026 HS_2056_B
	10	17.2	78.2	408	28	AZ536502	AZ536502 110300_96
	11	17.2	78.2	424	10	BE723539	BE723539 193384_MA
	12	17.2	78.2	463	9	AU083559	AU083559 AU083559
	13	17.2	78.2	479	9	AU089685	AU089685 AU089685
	14	17.2	78.2	513	12	BJ094274	BJ094274 BJ094274
	15	17.2	78.2	515	14	CF447937	CF447937 EST684282
	16	17.2	78.2	519	12	BI796581	BI796581 H049F08 E
	17	17.2	78.2	571	12	BM037907	BM037907 S114c07 S
	18	17.2	78.2	595	29	CC952473	CC952473 BOICU52TR
c	19	17.2	78.2	617	14	CD488495	CD488495 T10_D04 T
c	20	17.2	78.2	655	14	CD487922	CD487922 T02_B03 T
	21	17.2	78.2	726	13	BW071434	BW071434 BW071434
c	22	17.2	78.2	767	14	CB685128	CB685128 OSJNEf15E
c	23	17.2	78.2	812	14	CB644373	CB644373 OSJNEb05I
	24	17.2	78.2	844	14	CB685127	CB685127 OSJNEf15E
	25	17.2	78.2	882	14	CF378583	CF378583 AGENCOURT
c	26	17.2	78.2	972	29	CNS05PD9	AL347814 Tetraodon
	27	17.2	78.2	1028	13	CA139194	CA139194 SCEQRT209
c	28	17.2	78.2	2481	11	AK037625	AK037625 Mus muscu
	29	16.8	76.4	105	9	AA094019	AA094019 cl1619.se
c	30	16.8	76.4	496	29	CE537167	CE537167 tigr-gss-
	31	16.8	76.4	523	28	AZ483488	AZ483488 1M0309M12
	32	16.8	76.4	526	28	AZ501799	AZ501799 1M0340J17
c	33	16.8	76.4	628	14	CA380211	CA380211 659460 NC
	34	16.8	76.4	645	14	CB576172	CB576172 AMGNNUC:C
c	35	16.8	76.4	678	14	CA373611	CA373611 647793 NC
c	36	16.8	76.4	681	9	AV732648	AV732648 AV732648
	37	16.8	76.4	705	10	AW916461	AW916461 EST347765
	38	16.8	76.4	723	14	CB567509	CB567509 AGENCOURT
c	39	16.8	76.4	726	14	CA343200	CA343200 673263 NC
c	40	16.8	76.4	743	13	BU451759	BU451759 603771788
c	41	16.8	76.4	839	13	BU461599	BU461599 603772832
c	42	16.8	76.4	864	28	BH207673	BH207673 Sm1-57F15
	43	16.8	76.4	2923	28	BZ565411	BZ565411 pacs2-164
	44	16.4	74.5	222	14	CD069781	CD069781 MA2-0012T
c	45	16.4	74.5	367	29	CG399306	CG399306 ZMMBBc002

ALIGNMENTS

RESULT 1
BH859011
LOCUS BH859011 521 bp DNA linear GSS 13-NOV-2002
DEFINITION S5_182b_t7 Mouse Retroviral Tagged Cancer Gene Database Mus musculus genomic clone S5_182b, genomic survey sequence.
ACCESSION BH859011
VERSION BH859011.1 GI:21709832
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 521)
AUTHORS Suzuki,T., Shen,H., Akagi,K., Morse,H.C., Malley,J.D., Naiman,D.Q., Jenkins,N.A. and Copeland,N.G.
TITLE New genes involved in cancer identified by retroviral tagging
JOURNAL Nat. Genet. 32 (1), 166-174 (2002)
MEDLINE 22194816
PUBMED 12185365
COMMENT Contact: Copeland NG
Mouse Cancer Genetics Program
National Cancer Institute
Bldg. 539, Rm. 229, Frederick, MD 21702-1201, USA
Tel: 301 846 1260
Fax: 301 846 6666
Email: copeland@ncifcrf.gov
Class: PCR with specific primers.

```
FEATURES             Location/Qualifiers
     source          1. .521
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="S5_182b"
                     /sex="female"
                     /tissue_type="leukemia"
                     /clone_lib="Mouse Retroviral Tagged Cancer Gene Database"
                     /note="Inverse PCR method
                     (http://genome2.ncifcrf.gov/RTCGD)"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 28;  Length 521;
  Best Local Similarity   90.9%;  Pred. No. 2.1e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| | ||||||||
Db        116 TGACTGTGAACATGCGAGATGA 137


RESULT 2
BM042508
LOCUS       BM042508                571 bp    mRNA    linear   EST 07-NOV-2001
DEFINITION  603615795T1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420734 3',
            mRNA sequence.
ACCESSION   BM042508
VERSION     BM042508.1  GI:16771788
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1875  row: m  column: 23
            High quality sequence start: 44
            High quality sequence stop: 411.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5420734"
                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             83.6%;  Score 18.4;  DB 12;  Length 571;
  Best Local Similarity   95.0%;  Pred. No. 3.4e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGAT 20
              |||||||||||||||| ||||
Db        504 TGACTGTGAACGTTCTAGAT 523


RESULT 3
CE751403/c
LOCUS       CE751403                492 bp    DNA     linear   GSS 30-SEP-2003
DEFINITION  tigr-gss-dog-17000369615400 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE751403
VERSION     CE751403.1  GI:37092020
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 492)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
  MEDLINE   22875432
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .492
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

  Query Match             80.9%;  Score 17.8;  DB 29;  Length 492;
  Best Local Similarity   90.5%;  Pred. No. 6.2e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATG 21
              |||||||||||||| || ||||
Db         36 TGACTGTGAACGTGCGGGATG 16


RESULT 4
AZ755668/c
LOCUS       AZ755668                561 bp    DNA     linear   GSS 01-MAR-2001
DEFINITION  ev02g09.x1 PAX3 CASTing Library 'ev' Homo sapiens genomic clone
            ev02g09 random, genomic survey sequence.
ACCESSION   AZ755668
VERSION     AZ755668.1  GI:13175090
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Barber,T.D., Barber,M.C., Tomescu,O., Barr,F.G., Ruben,S. and
            Friedman,T.B.
  TITLE     Identification of Target Genes Regulated by PAX3 and PAX3--FKHR in
            Embryogenesis and Alveolar Rhabdomyosarcoma
  JOURNAL   Genomics 79 (3), 278-284 (2002)
  MEDLINE   21853298
   PUBMED   11863357
```

```
COMMENT     Contact: Friedman TB
            Laboratory of Molecular Genetics
            National Institute on Deafness and Other Communication Disorders,
            National Institutes of Health
            5 Research Court, Room 2A-15, Rockville, MD 20850, USA
            Tel: 301 402 7580
            Fax: 301 496 7882
            Email: friedman@nidcd.nih.gov
            Plate: 02  row: g  column: 09
            Seq primer: -21M13 forward primer (ABI)
            Class: random plasmid subclone.
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="ev02g09"
                     /sex="Male"
                     /lab_host="DH10B"
                     /clone_lib="PAX3 CASTing Library 'ev'"
                     /note="Vector: pGEM-T Easy; Human genomic DNA was
                     partially digested with Sau3AI, ligated to ds  linkers,
                     and enriched for binding to human PAX3dQ+ protein using a
                     Whole Genome PCR-based strategy.  DNA fragments containing
                     putative  PAX3dQ+ binding sites were amplified by PCR and
                     cloned into pGEM-T  Easy (Promega).  The ligation products
                     were transformed into DH10B  electrocompetent cells (Life
                     Technologies)."
ORIGIN

  Query Match             80.9%;  Score 17.8;  DB 28;  Length 561;
  Best Local Similarity   90.5%;  Pred. No. 6.5e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATG 21
              ||||||||||||  ||||||
Db        461 TGACTGTGAACGTCAGAGATG 441


RESULT 5
BZ558601
LOCUS       BZ558601                867 bp    DNA     linear   GSS 17-DEC-2002
DEFINITION  pa98401_292.s1 pacs2-164 Pseudomonas aeruginosa genomic clone
            pa98401_292, genomic survey sequence.
ACCESSION   BZ558601
VERSION     BZ558601.1  GI:27173329
KEYWORDS    GSS.
SOURCE      Pseudomonas aeruginosa
  ORGANISM  Pseudomonas aeruginosa
            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Pseudomonadaceae; Pseudomonas.
REFERENCE   1  (bases 1 to 867)
  AUTHORS   Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
            Burns,J.L., Kaul,R. and Olsen,M.V.
  TITLE     Whole-Genome-Sequence variation among multiple isolates of
            Psedomonas aeruginosa library
  JOURNAL   J. Bacteriol. (2002) In press
COMMENT     Contact: Chris K. Raymond
            Genome Center
            University of Washington
            Box 352145, Seattle, WA 98105-2145, USA
            Tel: 2062216954
            Fax: 2066857244
            Email: craymond@u.washington.edu
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .867
                     /organism="Pseudomonas aeruginosa"
                     /mol_type="genomic DNA"
                     /strain="2-164"
                     /db_xref="taxon:287"
                     /clone="pa98401_292"
                     /clone_lib="pacs2-164"
                     /note="clinical isolate 2-164 Whole genomic shotgun
                     library."
ORIGIN

  Query Match             80.9%;  Score 17.8;  DB 28;  Length 867;
  Best Local Similarity   90.5%;  Pred. No. 7.7e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GACTGTGAACGTTCGAGATGA 22
              ||||||||||  |||||  ||||
Db        724 GACTGTGAACCTTCGATATGA 744


RESULT 6
BF971856
LOCUS       BF971856                961 bp    mRNA    linear   EST 22-JAN-2001
DEFINITION  602240444F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4328890 5',
            mRNA sequence.
ACCESSION   BF971856
VERSION     BF971856.1  GI:12339071
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 961)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1189  row: h  column: 11
            High quality sequence stop: 555.
FEATURES             Location/Qualifiers
     source          1. .961
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4328890"
                     /tissue_type="leiomyosarcoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_46"
                     /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match             80.9%;  Score 17.8;  DB 10;  Length 961;
  Best Local Similarity   90.5%;  Pred. No. 8e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GACTGTGAACGTTCGAGATGA 22
              ||||||||||||  |||||
Db        650 GACTGTGAACGTTCCGGATGA 670


RESULT 7
AZ060178/c
LOCUS       AZ060178                489 bp    DNA     linear   GSS 30-MAR-2000
DEFINITION  RPCI-23-405E23.TJ RPCI-23 Mus musculus genomic clone
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            RPCI-23-405E23, genomic survey sequence.
ACCESSION   AZ060178
VERSION     AZ060178.1  GI:7351427
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 489)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-405E23.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 405  row: E  column: 23
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .489
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="RPCI-23-405E23"
                      /sex="Female"
                      /lab_host="DH10B"
                      /clone_lib="RPCI-23"
                      /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                      EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                      brain genomic DNA was isolated and  partially digested
                      with a combination of EcoRI and EcoRI Methylase.   Size
                      selected DNA was cloned into the pBACe3.6 vector at the
                      EcoRI  sites.  The ligation products were transformed into
                      DH10B  electrocompetent cells (BRL Life Technologies).   "
ORIGIN

  Query Match             79.1%;  Score 17.4;  DB 28;  Length 489;
  Best Local Similarity   94.7%;  Pred. No. 9.6e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGA 19
              |||||||||| |||||||
Db        170 TGACTGTGAACATTCGAGA 152


RESULT 8
AZ886419/c
LOCUS       AZ886419                 530 bp    DNA     linear   GSS 05-MAR-2001
DEFINITION  RPCI-23-182I6.TJ RPCI-23 Mus musculus genomic clone RPCI-23-182I6,
            genomic survey sequence.
ACCESSION   AZ886419
VERSION     AZ886419.1  GI:13205364
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 530)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-182I6.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 182  row: I  column: 6
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .530
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="RPCI-23-182I6"
                      /sex="Female"
                      /lab_host="DH10B"
                      /clone_lib="RPCI-23"
                      /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                      EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                      brain genomic DNA was isolated and  partially digested
                      with a combination of EcoRI and EcoRI Methylase.   Size
                      selected DNA was cloned into the pBACe3.6 vector at the
                      EcoRI  sites.  The ligation products were transformed into
                      DH10B  electrocompetent cells (BRL Life Technologies).   "
ORIGIN

  Query Match             79.1%;  Score 17.4;  DB 28;  Length 530;
  Best Local Similarity   94.7%;  Pred. No. 9.9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGA 19
              |||||||||| |||||||
Db        189 TGACTGTGAACATTCGAGA 171


RESULT 9
AQ245026
LOCUS       AQ245026                 374 bp    DNA     linear   GSS 03-OCT-1998
DEFINITION  HS_2056_B1_E03_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=2056 Col=5 Row=J, genomic survey
            sequence.
ACCESSION   AQ245026
VERSION     AQ245026.1  GI:3691600
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 374)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
```

```
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 2056  row: J  column: 5
            Class: BAC ends
            High quality sequence stop: 374.
FEATURES             Location/Qualifiers
     source          1. .374
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=2056 Col=5 Row=J"
                     /sex="male"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 28;  Length 374;
  Best Local Similarity   86.4%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||||| | ||||| |
Db        207 TGACTGTGAACGATTGAGATCA 228


RESULT 10
AZ536502
LOCUS       AZ536502                 408 bp    DNA     linear   GSS 03-NOV-2000
DEFINITION  110300_96 Planococcus lilacinus DNA Planococcus lilacinus genomic,
            genomic survey sequence.
ACCESSION   AZ536502
VERSION     AZ536502.1  GI:11093449
KEYWORDS    GSS.
SOURCE      Planococcus lilacinus (lilac mealybug)
  ORGANISM  Planococcus lilacinus
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Coccoidea; Pseudococcidae; Planococcus.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   Mohan,K.N. and Chandra,H.S.
  TITLE     Mealybug shotgun sequencing
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Mohan KN
            Microbiology and Cell Biology
            Indian Institute of Science
            Sir C.V. Raman Avenue, Bangalore, Karnataka 560012, India
            Email: mohan@mcbl.iisc.ernet.in
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .408
                     /organism="Planococcus lilacinus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:40930"
                     /clone_lib="Planococcus lilacinus DNA"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 28;  Length 408;
  Best Local Similarity   86.4%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||||| ||| ||||
Db        251 TGACTGTGAACGAACGATATGA 272


RESULT 11
BE723539
LOCUS       BE723539                 424 bp    mRNA    linear   EST 25-APR-2001
DEFINITION  193384 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BE723539
VERSION     BE723539.1  GI:10124826
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 424)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
            Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
            Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
   PUBMED   11282978
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 92  row: E  column: 14
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .424
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 4BOV"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from day 20 and day 40
                     embryos."
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 10;  Length 424;
  Best Local Similarity   86.4%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||| | |||||||| |||||||
Db        268 TGAGTCTGAACGTTAGAGATGA 289


RESULT 12
AU083559
LOCUS       AU083559                 463 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AU083559 Rice green shoot Oryza sativa (japonica cultivar-group)
            cDNA clone S14862, mRNA sequence.
ACCESSION   AU083559
VERSION     AU083559.1  GI:7274015
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 463)
  AUTHORS   Sasaki,T. and Yamamoto,K.
  TITLE     Rice cDNA from green shoot (2000)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takuji Sasaki
```

```
            National Institute of Agrobiological Resources
            Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
            305-8602, Japan
            Tel: 81-298-38-7441
            Fax: 81-298-38-7468
            Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
            PROJECT ='RGP'.
FEATURES              Location/Qualifiers
     source           1. .463
                      /organism="Oryza sativa (japonica cultivar-group)"
                      /mol_type="mRNA"
                      /cultivar="Nipponbare"
                      /db_xref="taxon:39947"
                      /clone="S14862"
                      /clone_lib="Rice green shoot"
                      /note="Green shoot (8 days old)"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 9;  Length 463;
  Best Local Similarity   86.4%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||| |||||| ||| |||||||
Db        151 TGAGTGTGAATGTTAGAGATGA 172


RESULT 13
AU089685
LOCUS       AU089685                479 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AU089685 Rice callus Oryza sativa (japonica cultivar-group) cDNA
            clone C40060, mRNA sequence.
ACCESSION   AU089685
VERSION     AU089685.1  GI:7652165
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 479)
  AUTHORS   Sasaki,T. and Yamamoto,K.
  TITLE     Rice cDNA from callus (2000)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takuji Sasaki
            National Institute of Agrobiological Resources
            Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
            305-8602, Japan
            Tel: 81-298-38-7441
            Fax: 81-298-38-7468
            Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
            PROJECT ='RGP'.
FEATURES              Location/Qualifiers
     source           1. .479
                      /organism="Oryza sativa (japonica cultivar-group)"
                      /mol_type="mRNA"
                      /cultivar="Nipponbare"
                      /db_xref="taxon:39947"
                      /clone="C40060"
                      /clone_lib="Rice callus"
                      /note="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
                      NotI; cDNA prepared from rice callus mRNAs by using
                      oligo(dT) as a primer and ligating to the SalI-NotI site
                      of pBluescript II SK+ phagemid.  "
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 9;  Length 479;
  Best Local Similarity   86.4%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||| |||||| ||| |||||||
Db        299 TGAGTGTGAATGTTAGAGATGA 320


RESULT 14
BJ094274
LOCUS       BJ094274                513 bp    mRNA    linear   EST 01-OCT-2003
DEFINITION  BJ094274 NIBB Mochii normalized Xenopus early gastrula library
            Xenopus laevis cDNA clone XL144p18 5', mRNA sequence.
ACCESSION   BJ094274
VERSION     BJ094274.1  GI:17594227
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 513)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .513
                      /organism="Xenopus laevis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8355"
                      /clone="XL144p18"
                      /tissue_type="whole embryo"
                      /dev_stage="stage 10.5"
                      /clone_lib="NIBB Mochii normalized Xenopus early gastrula
                      library"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 12;  Length 513;
  Best Local Similarity   86.4%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              || ||| |||||||||| |||||
Db        198 TGCCTGAGAACGTTCGCGATGA 219


RESULT 15
CF447937
LOCUS       CF447937                515 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  EST684282 normalized cDNA library of onion Allium cepa cDNA clone
            ACABF87, mRNA sequence.
ACCESSION   CF447937
VERSION     CF447937.1  GI:34470639
KEYWORDS    EST.
SOURCE      Allium cepa (onion)
  ORGANISM  Allium cepa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
            Allium.
REFERENCE   1  (bases 1 to 515)
  AUTHORS   Havey,M.J., Cheung,F., Van Aken,S., Utterback,T. and Town,C.D.
  TITLE     Expressed Sequence Tags from a normalized library of mixed onion
            tissues (Allium cepa)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Havey MJ
            Department of Horticulture
            USDA-ARS and University of Wisconsin
            1575 Linden Drive, Madison, WI 53706, USA
```

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            Tel: 608-262-1830
            Fax: 608-262-4743
            Email: mjhavey@facstaff.wisc.edu
            TIGR sequence name ACABF87TR. For more information:
            http://haveylab.hort.wisc.edu
            Seq primer: CAG GAA ACA GCT ATG ACC.
FEATURES              Location/Qualifiers
     source           1. .515
                      /organism="Allium cepa"
                      /mol_type="mRNA"
                      /cultivar="Red Creole(bulbs), unknown(callus), Ebano &
                      Texas Legend(roots)"
                      /db_xref="taxon:4679"
                      /clone="ACABF87"
                      /tissue_type="Callus, roots, and young bulbs"
                      /clone_lib="normalized cDNA library of onion"
                      /note="Vector: pCMVSport6.1-ccdb (Invitrogen); Site_1:
                      EcoRV (5'); Site_2: NotI (3'); Equal molar amounts of mRNA
                      from callus, roots, and young bulbs were combined to
                      synthesize the library. Normalization to enrich for
                      low-copy transcripts was performed by proprietary
                      techniques of Invitrogen."
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 14;  Length 515;
  Best Local Similarity   86.4%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||  | ||||||||||
Db         10 TGACTGTTGATGTTCGAGATGA 31


RESULT 16
BI796581
LOCUS       BI796581                519 bp    mRNA    linear   EST 02-OCT-2001
DEFINITION  H049F08 Endosperm library from Oryza sativa (10 days after
            anthesis) Oryza sativa cDNA clone H049F08, mRNA sequence.
ACCESSION   BI796581
VERSION     BI796581.1  GI:15848305
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 519)
  AUTHORS   Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X.,
            Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
  TITLE     A Gene Expression Screen in Oryza sativa
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Haitao Dong, Debao Li
            Bioinfomatics and Gene Network Research Group
            Zhejiang University
            Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
            Tel: 0086-571-86892051
            Fax: 0086-571-86961525
            Email: webmaster@estarray.org, URL: http://www.estarray.org
            Seq primer: M13 forward primer.
FEATURES              Location/Qualifiers
     source           1. .519
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /db_xref="taxon:4530"
                      /clone="H049F08"
                      /tissue_type="Endosperm"
                      /dev_stage="10 days after anthesis"
                      /clone_lib="Endosperm library from Oryza sativa (10 days
                      after anthesis)"
                      /note="Vector: pSport2"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 12;  Length 519;
  Best Local Similarity   86.4%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||  ||||||  |||  |||||||
Db        266 TGAGTGTGAATGTTAGAGATGA 287


RESULT 17
BM037907
LOCUS       BM037907                571 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  S114c07 Stem library from Oryza sativa (3-5 leaf stage) Oryza
            sativa cDNA clone S114c07, mRNA sequence.
ACCESSION   BM037907
VERSION     BM037907.1  GI:16753528
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X.,
            Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
  TITLE     A Gene Expression Screen in Oryza sativa
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Haitao Dong, Debao Li
            Bioinfomatics and Gene Network Research Group
            Zhejiang University
            Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
            Tel: 0086-571-86892051
            Fax: 0086-571-86961525
            Email: webmaster@estarray.org, URL: http://www.estarray.org
            Seq primer: M13 forward primer.
FEATURES              Location/Qualifiers
     source           1. .571
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /db_xref="taxon:4530"
                      /clone="S114c07"
                      /tissue_type="Stem"
                      /dev_stage="3-5 leaf stage"
                      /clone_lib="Stem library from Oryza sativa (3-5 leaf
                      stage)"
                      /note="Vector: pSport2"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 12;  Length 571;
  Best Local Similarity   86.4%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||  ||||||  |||  |||||||
Db        179 TGAGTGTGAATGTTAGAGATGA 200


RESULT 18
CC952473
LOCUS       CC952473                595 bp    DNA     linear   GSS 18-AUG-2003
DEFINITION  BOICU52TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
            BOICU52, genomic survey sequence.
ACCESSION   CC952473
VERSION     CC952473.1  GI:33791266
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 595)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
```

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COMMENT     Other_GSSs: BOICU52TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .595
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOICU52"
                     /clone_lib="BO_1.4_1.6_KB_nuc"
                     /note="Vector: pHOS2; Site_1: BstXI; 1.4-1.6 kb sheared
                     nuclear DNA inserted into pHOS2 using BstXI linkers"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 29;  Length 595;
  Best Local Similarity   86.4%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||  |||||||||  |
Db        210 TGACTGTGATTGTTCGAGATTA 231


RESULT 19
CD488495/c
LOCUS       CD488495                617 bp    mRNA    linear   EST 29-AUG-2003
DEFINITION  T10_D04 Teliospore Ustilago maydis cDNA 5', mRNA sequence.
ACCESSION   CD488495
VERSION     CD488495.1  GI:34330993
KEYWORDS    EST.
SOURCE      Ustilago maydis
  ORGANISM  Ustilago maydis
            Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
            Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   Sacadura,N.T. and Saville,B.J.
  TITLE     Gene expression and EST analyses of Ustilago maydis germinating
            teliospores
  JOURNAL   Fungal Genet. Biol. 40 (1), 47-64 (2003)
  MEDLINE   22829673
   PUBMED   12948513
COMMENT     Contact: Barry J. Saville
            Saville Lab
            University of Toronto
            3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
            Tel: 905 569 4702
            Fax: 905 828 3792
            Email: bsaville@utm.utoronto.ca
            Seq primer: M13 reverse primer (5' AAACAGCTATGACCATGTTCA 3').
FEATURES             Location/Qualifiers
     source          1. .617
                     /organism="Ustilago maydis"
                     /mol_type="mRNA"
                     /strain="FB1/FB2"
                     /db_xref="taxon:5270"
                     /cell_type="Teliospore"
                     /dev_stage="Germinating teliospore"
                     /lab_host="E. coli"
                     /clone_lib="Teliospore"
                     /note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB;
                     mRNA was extracted from germinating teliospores. cDNA was
                     amplified by PCR and unidirectionally cloned into pDNR-LIB
                     plasmid, with the use of Clontech's Creator SMART cDNA
                     Library Construction Kit."
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 14;  Length 617;
  Best Local Similarity   86.4%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||| | ||||||||||| |||
Db        439 TGACCGGGAACGTTCGAGTTGA 418


RESULT 20
CD487922/c
LOCUS       CD487922                655 bp    mRNA    linear   EST 29-AUG-2003
DEFINITION  T02_B03 Teliospore Ustilago maydis cDNA 5', mRNA sequence.
ACCESSION   CD487922
VERSION     CD487922.1  GI:34330420
KEYWORDS    EST.
SOURCE      Ustilago maydis
  ORGANISM  Ustilago maydis
            Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
            Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE   1  (bases 1 to 655)
  AUTHORS   Sacadura,N.T. and Saville,B.J.
  TITLE     Gene expression and EST analyses of Ustilago maydis germinating
            teliospores
  JOURNAL   Fungal Genet. Biol. 40 (1), 47-64 (2003)
  MEDLINE   22829673
   PUBMED   12948513
COMMENT     Contact: Barry J. Saville
            Saville Lab
            University of Toronto
            3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
            Tel: 905 569 4702
            Fax: 905 828 3792
            Email: bsaville@utm.utoronto.ca
            Seq primer: M13 reverse primer (5' AAACAGCTATGACCATGTTCA 3').
FEATURES             Location/Qualifiers
     source          1. .655
                     /organism="Ustilago maydis"
                     /mol_type="mRNA"
                     /strain="FB1/FB2"
                     /db_xref="taxon:5270"
                     /cell_type="Teliospore"
                     /dev_stage="Germinating teliospore"
                     /lab_host="E. coli"
                     /clone_lib="Teliospore"
                     /note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB;
                     mRNA was extracted from germinating teliospores. cDNA was
                     amplified by PCR and unidirectionally cloned into pDNR-LIB
                     plasmid, with the use of Clontech's Creator SMART cDNA
                     Library Construction Kit."
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 14;  Length 655;
  Best Local Similarity   86.4%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||| | ||||||||||| |||
Db        408 TGACCGGGAACGTTCGAGTTGA 387


RESULT 21
BW071434
LOCUS       BW071434                726 bp    mRNA    linear   EST 20-OCT-2002
DEFINITION  BW071434 Nori Satoh unpublished cDNA library, cleaving embryo Ciona
            intestinalis cDNA clone rciclo96b23 3', mRNA sequence.
ACCESSION   BW071434
VERSION     BW071434.1  GI:24172846
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
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            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 726)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .726
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcic1096b23"
                     /tissue_type="whole body"
                     /dev_stage="cleaving embryo"
                     /clone_lib="Nori Satoh unpublished cDNA library, cleaving
                     embryo"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 13;  Length 726;
  Best Local Similarity   86.4%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||| ||  ||||
Db         17 TGACTGTGAACGTGCGGTATGA 38


RESULT 22
CB685128/c
LOCUS       CB685128                767 bp    mRNA    linear   EST 09-APR-2003
DEFINITION  OSJNEf15E19.r OSJNEf Oryza sativa (japonica cultivar-group) cDNA
            clone OSJNEf15E19 3', mRNA sequence.
ACCESSION   CB685128
VERSION     CB685128.1  GI:29688853
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 767)
  AUTHORS   Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
            Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
  TITLE     Large-scale identification of ESTs involved in the interaction
            between rice and Magnaporthe grisea
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
            PCR PRimers
            FORWARD: gta aaa cga cgg cca gtg
            BACKWARD: gga aac agc tat gac cat g
            Plate: 15  row: E  column: 19
            Seq primer: gga aac agc tat gac cat g.
FEATURES             Location/Qualifiers
     source          1. .767
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="OSJNEf15E19"
                     /tissue_type="Leaf"
                     /dev_stage="3 week"
                     /lab_host="DH10B"
                     /clone_lib="OSJNEf"
                     /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
                     XhoI; Uninfected Control"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 14;  Length 767;
  Best Local Similarity   86.4%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||| |||||| ||| |||||||
Db        215 TGAGTGTGAATGTTAGAGATGA 194


RESULT 23
CB644373/c
LOCUS       CB644373                812 bp    mRNA    linear   EST 08-APR-2003
DEFINITION  OSJNEb05I22.r OSJNEb Oryza sativa (japonica cultivar-group) cDNA
            clone OSJNEb05I22 3', mRNA sequence.
ACCESSION   CB644373
VERSION     CB644373.1  GI:29639364
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 812)
  AUTHORS   Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
            Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
  TITLE     Large-scale identification of ESTs involved in the interaction
            between rice and Magnaporthe grisea
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
            PCR PRimers
            FORWARD: gta aaa cga cgg cca gtg
            BACKWARD: gga aac agc tat gac cat g
            Plate: 05  row: I  column: 22
            Seq primer: gga aac agc tat gac cat g.
FEATURES             Location/Qualifiers
     source          1. .812
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="OSJNEb05I22"
                     /tissue_type="Leaf"
                     /dev_stage="3 week"
                     /lab_host="DH10B"
                     /clone_lib="OSJNEb"
                     /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
                     XhoI; 24 hrs after innoculation with Rice Blast (Che
                     86061)"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 14;  Length 812;
  Best Local Similarity   86.4%;  Pred. No. 1.5e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||| |||||| ||| |||||||
Db        372 TGAGTGTGAATGTTAGAGATGA 351
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RESULT 24
CB685127
LOCUS       CB685127                844 bp    mRNA    linear   EST 09-APR-2003
DEFINITION  OSJNEf15E19.f OSJNEf Oryza sativa (japonica cultivar-group) cDNA
            clone OSJNEf15E19 5', mRNA sequence.
ACCESSION   CB685127
VERSION     CB685127.1  GI:29688852
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 844)
  AUTHORS   Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
            Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
  TITLE     Large-scale identification of ESTs involved in the interaction
            between rice and Magnaporthe grisea
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
            PCR PRimers
            FORWARD: gta aaa cga cgg cca gtg
            BACKWARD: gga aac agc tat gac cat g
            Plate: 15  row: E  column: 19
            Seq primer: gta aaa cga cgg cca gtg.
FEATURES             Location/Qualifiers
     source          1. .844
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="OSJNEf15E19"
                     /tissue_type="Leaf"
                     /dev_stage="3 week"
                     /lab_host="DH10B"
                     /clone_lib="OSJNEf"
                     /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
                     XhoI; Uninfected Control"
ORIGIN

  Query Match            78.2%;  Score 17.2;  DB 14;  Length 844;
  Best Local Similarity  86.4%;  Pred. No. 1.5e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||| |||||| ||| |||||||
Db        807 TGAGTGTGAATGTTAGAGATGA 828


RESULT 25
CF378583
LOCUS       CF378583                882 bp    mRNA    linear   EST 27-AUG-2003
DEFINITION  AGENCOURT_15341601 NICHD_XGC_Swb1N Silurana tropicalis cDNA clone
            IMAGE:7005347 5', mRNA sequence.
ACCESSION   CF378583
VERSION     CF378583.1  GI:34316027
KEYWORDS    EST.
SOURCE      Silurana tropicalis (western clawed frog)
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 882)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Rob Granger, University of Virginia
             cDNA Library Preparation: Open Biosystems
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14704  row: c  column: 09
            High quality sequence stop: 610.
FEATURES             Location/Qualifiers
     source          1. .882
                     /organism="Silurana tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:7005347"
                     /tissue_type="whole body"
                     /clone_lib="NICHD_XGC_Swb1N"
                     /note="Vector: pExpress-1; Site_1: EcoRV; Site_2: NotI;
                     Bulk tissue was collected from a whole 10 month old male
                     from the F6 strain. 1st strand cDNA was primed with a Not
                     I - oligo(dT) primer, double-stranded cDNA was cloned into
                     the Not I and EcoRV sites of pExpress-1. Library was
                     size-selected for >1.5 kb fragments for an average insert
                     size of 1.92 kb. Library was normalized to Cot5 with a
                     180-fold reduction of actin. A non-normalized version of
                     this library is also available (NICHD_XGC_Swb1). Library
                     was constructed by Open Biosystems (Huntsville, AL)."
ORIGIN

  Query Match            78.2%;  Score 17.2;  DB 14;  Length 882;
  Best Local Similarity  86.4%;  Pred. No. 1.5e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||| |||||| ||| |||||||
Db        137 TGACTGTAAAGGTTCTAGATGA 158


RESULT 26
CNS05PD9/c
LOCUS       CNS05PD9                972 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            005F08 of library A from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL347814
VERSION     AL347814.1  GI:8241584
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
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  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 972)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .972
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="005F08"
                     /clone_lib="A"
                     /note="Genoscope sequence ID : C0AA005DC04C1~end : T7"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 29;  Length 972;
  Best Local Similarity   86.4%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              || ||||||| || ||||||||
Db         46 TGGCTGTGAAGGTGCGAGATGA 25


RESULT 27
CA139194
LOCUS       CA139194                1028 bp    mRNA    linear   EST 24-SEP-2003
DEFINITION  SCEQRT2094G05.g RT2 Saccharum officinarum cDNA clone SCEQRT2094G05
            5', mRNA sequence.
ACCESSION   CA139194
VERSION     CA139194.1  GI:35030936
KEYWORDS    EST.
SOURCE      Saccharum officinarum
  ORGANISM  Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE   1  (bases 1 to 1028)
  AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
  TITLE     The libraries that made SUCEST
  JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT     Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bcccenter.fcav.unesp.br
            Plate: 094  row: G  column: 05
            Seq primer: T7 Promoter Primer.
FEATURES             Location/Qualifiers
     source          1. .1028
                     /organism="Saccharum officinarum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4547"
                     /clone="SCEQRT2094G05"
                     /lab_host="DH10B"
                     /clone_lib="RT2"
                     /note="Organ: Root tips(0.3cm-long) from adult plants;
                     Vector: pSport1; Site_1: SalI; Site_2: NotI; An
                     unidirectional cDNA library generated from [Root
                     tips(0.3cm-long) from  adult plants]. cDNA was prepared
                     from polyA+ mRNA using SuperScript  Plasmid System Kit
                     (Invitrogen). The double-strand cDNAs were  fractionated
                     in a sepharose CL-2B 40cm-columns and fragments sizing
                     between 0.8 and 1.5 Kb were directionally cloned into the
                     vector. Details  of each source of RNA and library
                     construction can be obtained at
                     http://sucest.lad.ic.unicamp.br/public"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 13;  Length 1028;
  Best Local Similarity   86.4%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| ||||| | |||
Db        626 TGACTGTGAAGGTTCGTGGTGA 647


RESULT 28
AK037625/c
LOCUS       AK037625                2481 bp    mRNA    linear   HTC 19-SEP-2003
DEFINITION  Mus musculus 16 days neonate thymus cDNA, RIKEN full-length
            enriched library, clone:A130030F17 product:unknown EST, full insert
            sequence.
ACCESSION   AK037625
VERSION     AK037625.1  GI:26085966
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2481)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
     source          1. .2481
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:A130030F17"
                     /db_xref="MGI:2402091"
                     /db_xref="taxon:10090"
                     /clone="A130030F17"
                     /tissue_type="thymus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="16 days neonate"
     misc_feature    1. .2481
                     /note="unknown EST (GB|BE692239, evidence: BLASTN, 99%,
                     match=501)"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 11;  Length 2481;
  Best Local Similarity   86.4%;  Pred. No. 2.3e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||| ||||||| || ||||||||
Db        605 TGAATGTGAACTTTGGAGATGA 584


RESULT 29
AA094019
LOCUS       AA094019                105 bp    mRNA    linear   EST 25-OCT-1996
DEFINITION  cl1619.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
            cDNA 5', mRNA sequence.
ACCESSION   AA094019
VERSION     AA094019.1  GI:1639612
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 105)
  AUTHORS   Liew,C.C.
  TITLE     cDNAs from fetal heart (1996)
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Liew CC
            Brigham and Women's Hospital
            Harvard Medical School
            75 Francis St. Boston, MA 02115, USA
            Tel: 6177328915
            Fax: 6179750995
            Email: cliew@rics.bwh.harvard.edu
            PCR PRimers
            FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
            BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
            Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
FEATURES             Location/Qualifiers
     source          1. .105
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /lab_host="E. coli XL1-Blue"
                     /clone_lib="Human fetal heart, Lambda ZAP Express"
                     /note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
                     XhoI; mRNA was purified from human fetal hearts (8-10
                     weeks). cDNA was synthesized using a XhoI-Oligo dT
                     adaptor-primer. EcoRI adaptors were ligated, followed by
                     digestion with XhoI, for directional cloning into
                     predigested lambda ZAP Express."
ORIGIN

  Query Match             76.4%;  Score 16.8;  DB 9;  Length 105;
  Best Local Similarity   90.0%;  Pred. No. 1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGAT 20
              |||||||||| ||| ||||
Db         43 TGACTGTGAACCTTCCAGAT 62


RESULT 30
CE537167/c
LOCUS       CE537167                496 bp    DNA     linear   GSS 28-SEP-2003
DEFINITION  tigr-gss-dog-17000365936856 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE537167
VERSION     CE537167.1  GI:36853948
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 496)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
  MEDLINE   22875432
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .496
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

  Query Match             76.4%;  Score 16.8;  DB 29;  Length 496;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ACTGTGAACGTTCGAGATGA 22
```

```
Db        184 ACTGTGAAGGATCGAGATGA 165
```

RESULT 31
AZ483488
LOCUS AZ483488 523 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0309M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0309M12 F, genomic survey sequence.
ACCESSION AZ483488
VERSION AZ483488.1 GI:10647510
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 523)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0309 row: M column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 523.

FEATURES Location/Qualifiers
source 1. .523
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0309M12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 76.4%; Score 16.8; DB 28; Length 523;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 ACTGTGAACGTTCGAGATGA 22
```

```
Db        376 ACTGTGTACTTTCGAGATGA 395
```

RESULT 32
AZ501799
LOCUS AZ501799 526 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0340J17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0340J17 R, genomic survey sequence.
ACCESSION AZ501799
VERSION AZ501799.1 GI:10683115
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 526)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0340 row: J column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 526.

FEATURES Location/Qualifiers
source 1. .526
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0340J17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 76.4%; Score 16.8; DB 28; Length 526;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 TGACTGTGAACGTTCGAGAT 20
```

```
                    |||| |||||||||| ||||
Db          60 TGACAGTGAACGTTCTAGAT 79


RESULT 33
CA380211/c
LOCUS       CA380211                628 bp    mRNA    linear   EST 06-NOV-2002
DEFINITION  659460 NCCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT49D04_D_B02 5',
            mRNA sequence.
ACCESSION   CA380211
VERSION     CA380211.1  GI:24701684
KEYWORDS    EST.
SOURCE      Oncorhynchus mykiss (rainbow trout)
  ORGANISM  Oncorhynchus mykiss
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE   1  (bases 1 to 628)
  AUTHORS   Rexroad,C.E. and Keele,J.W.
  TITLE     Sequence analysis of a rainbow trout normalized cDNA library
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Rexroad CE
            USDA, ARS, National Center for Cool and Cold Water Aquaculture
            11876 Leetown Road, Kearneysville, WV 25430, USA
            Tel: 304 724 8340 x2129
            Fax: 304 725 0351
            Email: crexroad@ncccwa.ars.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified by
            cross_match v0.990329.
            Seq primer: AGCGGATAACAATTTCACACAGGA.
FEATURES             Location/Qualifiers
     source          1. .628
                     /organism="Oncorhynchus mykiss"
                     /mol_type="mRNA"
                     /db_xref="taxon:8022"
                     /clone="1RT49D04_D_B02"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="NCCCWA 1RT"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from brain, gill, liver,
                     spleen, muscle, and kidney."
ORIGIN

  Query Match             76.4%;  Score 16.8;  DB 14;  Length 628;
  Best Local Similarity   90.0%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ACTGTGAACGTTCGAGATGA 22
              |||| ||||| |||||||||
Db        138 ACTGAGAACGGTCGAGATGA 119


RESULT 34
CB576172
LOCUS       CB576172                645 bp    mRNA    linear   EST 03-APR-2003
DEFINITION  AMGNNUC:CDRG1-00006-H1-A cdrg1 (10898) Rattus norvegicus cDNA clone
            cdrg1-00006-h1 5', mRNA sequence.
ACCESSION   CB576172
VERSION     CB576172.1  GI:29520213
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 645)
  AUTHORS   Amgen EST Program.
  TITLE     Amgen Rat EST Program
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Dan Fitzpatrick
            Amgen, Inc
            One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
            Tel: 805 447-4881
            Plate: 00006  row: h  column: 1.
FEATURES             Location/Qualifiers
     source          1. .645
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="cdrg1-00006-h1"
                     /tissue_type="Chung Model Ipsilate"
                     /clone_lib="cdrg1 (10898)"
                     /note="Vector: pSPORT1; Chung Model Rat DRG Left L5/L6"
ORIGIN

  Query Match             76.4%;  Score 16.8;  DB 14;  Length 645;
  Best Local Similarity   90.0%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ACTGTGAACGTTCGAGATGA 22
              |||||| || ||||||||||
Db        424 ACTGTGGACCTTCGAGATGA 443


RESULT 35
CA373611/c
LOCUS       CA373611                678 bp    mRNA    linear   EST 06-NOV-2002
DEFINITION  647793 NCCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT14J21_B_E11 5',
            mRNA sequence.
ACCESSION   CA373611
VERSION     CA373611.1  GI:24689229
KEYWORDS    EST.
SOURCE      Oncorhynchus mykiss (rainbow trout)
  ORGANISM  Oncorhynchus mykiss
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   Rexroad,C.E. and Keele,J.W.
  TITLE     Sequence analysis of a rainbow trout normalized cDNA library
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Rexroad CE
            USDA, ARS, National Center for Cool and Cold Water Aquaculture
            11876 Leetown Road, Kearneysville, WV 25430, USA
            Tel: 304 724 8340 x2129
            Fax: 304 725 0351
            Email: crexroad@ncccwa.ars.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified by
            cross_match v0.990329.
            Seq primer: AGCGGATAACAATTTCACACAGGA.
FEATURES             Location/Qualifiers
     source          1. .678
                     /organism="Oncorhynchus mykiss"
                     /mol_type="mRNA"
                     /db_xref="taxon:8022"
                     /clone="1RT14J21_B_E11"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="NCCCWA 1RT"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from brain, gill, liver,
                     spleen, muscle, and kidney."
ORIGIN

  Query Match             76.4%;  Score 16.8;  DB 14;  Length 678;
  Best Local Similarity   90.0%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ACTGTGAACGTTCGAGATGA 22
              |||| ||||| |||||||||
Db        207 ACTGAGAACGGTCGAGATGA 188
```

RESULT 36
AV732648/c
LOCUS AV732648 681 bp mRNA linear EST 17-OCT-2000
DEFINITION AV732648 HTF Homo sapiens cDNA clone HTFBLB03 5', mRNA sequence.
ACCESSION AV732648
VERSION AV732648.1 GI:10850193
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 681)
AUTHORS Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
TITLE Homo sapiens cDNA HTF clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES Location/Qualifiers
source 1. .681
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HTFBLB03"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="HTF"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"
ORIGIN

Query Match 76.4%; Score 16.8; DB 9; Length 681;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ACTGTGAACGTTCGAGATGA 22
||||||||| || |||||||
Db 382 ACTGTGAACATTTGAGATGA 363

RESULT 37
AW916461
LOCUS AW916461 705 bp mRNA linear EST 25-MAY-2000
DEFINITION EST347765 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIDQ49 5' end, mRNA sequence.
ACCESSION AW916461
VERSION AW916461.1 GI:8082187
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 705)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC tel#703-365-2700 for further information
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .705
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="RGIDQ49"
/tissue_type="mix - brain, ovary, placenta, kidney, lung, liver, embryo, heart, muscle, spleen"
/lab_host="SOLR"
/clone_lib="Rat gene index, normalized rat, norvegicus, Bento Soares"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; Estimated insert size approx.1 kb"
ORIGIN

Query Match 76.4%; Score 16.8; DB 10; Length 705;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ACTGTGAACGTTCGAGATGA 22
||||||||| || |||||||
Db 150 ACTGTGGACCTTCGAGATGA 169

RESULT 38
CB567509
LOCUS CB567509 723 bp mRNA linear EST 02-APR-2003
DEFINITION AGENCOURT_12621670 NICHD_Rr_Pit1 Rattus norvegicus cDNA clone IMAGE:6922293 5', mRNA sequence.
ACCESSION CB567509
VERSION CB567509.1 GI:29487039
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 723)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: John C. Marshall, M.D., Ph.D
cDNA Library Preparation: CLONTECH
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM3177 row: j column: 20
High quality sequence stop: 538.
FEATURES Location/Qualifiers
source 1. .723
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:6922293"
/tissue_type="Pitutary"
/lab_host="DH10B"
/clone_lib="NICHD_Rr_Pit1"
/note="Vector: pDNR-LIB; Site_1: SfiI; Site_2: SfiI; 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.23 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for

full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
ORIGIN

Query Match 76.4%; Score 16.8; DB 14; Length 723;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ACTGTGAACGTTCGAGATGA 22
|||||| || ||||||||||
Db 165 ACTGTGGACCTTCGAGATGA 184

RESULT 39
CA343200/c
LOCUS CA343200 726 bp mRNA linear EST 05-NOV-2002
DEFINITION 673263 NCCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT68D07_B_B04 5', mRNA sequence.
ACCESSION CA343200
VERSION CA343200.1 GI:24588362
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 726)
AUTHORS Rexroad,C.E. and Keele,J.W.
TITLE Sequence analysis of a rainbow trout normalized cDNA library
JOURNAL Unpublished (2002)
COMMENT Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified by cross_match v0.990329.
Seq primer: AGCGGATAACAATTTCACACAGGA.
FEATURES Location/Qualifiers
source 1. .726
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="1RT68D07_B_B04"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="NCCCWA 1RT"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from brain, gill, liver, spleen, muscle, and kidney."
ORIGIN

Query Match 76.4%; Score 16.8; DB 14; Length 726;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ACTGTGAACGTTCGAGATGA 22
|||| ||||| |||||||||
Db 491 ACTGAGAACGGTCGAGATGA 472

RESULT 40
BU451759/c
LOCUS BU451759 743 bp mRNA linear EST 29-NOV-2002
DEFINITION 603771788F1 CSEQRBN14 Gallus gallus cDNA clone ChEST706o22 5', mRNA sequence.
ACCESSION BU451759
VERSION BU451759.1 GI:25941070
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 743)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
FEATURES Location/Qualifiers
source 1. .743
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="ChEST706o22"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRBN14"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
ORIGIN

Query Match 76.4%; Score 16.8; DB 13; Length 743;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GACTGTGAACGTTCGAGATG 21
|||||||||| || ||||||
Db 163 GACTGTGAACTTTTGAGATG 144

Search completed: April 24, 2004, 17:01:00
Job time : 2705.13 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 13:53:33 ; Search time 574.133 Seconds
(without alignments)
603.944 Million cell updates/sec

Title: US-09-802-445-1_COPY_9_16
Perfect score: 8
Sequence: 1 aacgttcg 8

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
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22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	8	100.0	8	6	AX104477	AX104477 Sequence
c	2	8	100.0	8	6	AX355157	AX355157 Sequence
c	3	8	100.0	8	6	AX547530	AX547530 Sequence
	4	8	100.0	10	6	AX592373	AX592373 Sequence
	5	8	100.0	10	6	AX592374	AX592374 Sequence
	6	8	100.0	10	6	AX592377	AX592377 Sequence
	7	8	100.0	10	6	AX592382	AX592382 Sequence
	8	8	100.0	10	6	AX592387	AX592387 Sequence
c	9	8	100.0	10	6	AX592387	AX592387 Sequence
	10	8	100.0	10	6	AX592389	AX592389 Sequence
	11	8	100.0	10	6	AX592390	AX592390 Sequence
	12	8	100.0	10	6	AX592391	AX592391 Sequence
	13	8	100.0	10	6	AX592392	AX592392 Sequence
	14	8	100.0	11	6	AX592412	AX592412 Sequence
c	15	8	100.0	11	6	AX592412	AX592412 Sequence
	16	8	100.0	11	6	AX592424	AX592424 Sequence
	17	8	100.0	12	6	AR176675	AR176675 Sequence
	18	8	100.0	12	6	BD260026	BD260026 Hybridiza
c	19	8	100.0	12	6	AR437498	AR437498 Sequence
	20	8	100.0	12	6	AX592417	AX592417 Sequence
	21	8	100.0	12	6	AX592419	AX592419 Sequence
	22	8	100.0	13	6	AX592407	AX592407 Sequence
c	23	8	100.0	13	6	AX592407	AX592407 Sequence
	24	8	100.0	13	6	AX592409	AX592409 Sequence
c	25	8	100.0	13	6	AX592409	AX592409 Sequence
	26	8	100.0	13	6	AX592411	AX592411 Sequence
	27	8	100.0	13	6	AX592413	AX592413 Sequence
	28	8	100.0	13	6	AX592422	AX592422 Sequence
	29	8	100.0	14	6	AR148617	AR148617 Sequence
	30	8	100.0	14	6	AX592408	AX592408 Sequence
c	31	8	100.0	14	6	AX592408	AX592408 Sequence
	32	8	100.0	14	6	AX592410	AX592410 Sequence
	33	8	100.0	14	6	AX592425	AX592425 Sequence
	34	8	100.0	14	6	AX592428	AX592428 Sequence
	35	8	100.0	14	6	BD136184	BD136184 Inhibitor
	36	8	100.0	15	6	AX592418	AX592418 Sequence
c	37	8	100.0	15	6	AX663401	AX663401 Sequence
	38	8	100.0	16	6	AR176673	AR176673 Sequence
	39	8	100.0	16	6	BD260024	BD260024 Hybridiza
	40	8	100.0	16	6	AX194461	AX194461 Sequence
	41	8	100.0	16	6	AX465411	AX465411 Sequence
	42	8	100.0	16	6	AX592321	AX592321 Sequence
c	43	8	100.0	16	6	AX592321	AX592321 Sequence
	44	8	100.0	16	6	AX592423	AX592423 Sequence
	45	8	100.0	16	6	AX592427	AX592427 Sequence

ALIGNMENTS

RESULT 1
AX104477/c
LOCUS AX104477 8 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 669 from Patent WO0122972.
ACCESSION AX104477
VERSION AX104477.1 GI:13920674
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 8)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 669 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical

GmbH (DE)
FEATURES Location/Qualifiers
source 1. .8
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 100.0%; Score 8; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.2e+09;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 8 AACGTTCG 1

RESULT 2
AX355157/c
LOCUS AX355157 8 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 185 from Patent WO0197843.
ACCESSION AX355157
VERSION AX355157.1 GI:18619824
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 185 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source 1. .8
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphodiester backbone"
ORIGIN

Query Match 100.0%; Score 8; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.2e+09;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 8 AACGTTCG 1

RESULT 3
AX547530/c
LOCUS AX547530 8 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 669 from Patent WO02053141.
ACCESSION AX547530
VERSION AX547530.1 GI:25812674
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 669 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES Location/Qualifiers
source 1. .8
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
ORIGIN

Query Match 100.0%; Score 8; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.2e+09;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 8 AACGTTCG 1

RESULT 4
AX592373
LOCUS AX592373 10 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 63 from Patent WO02052002.
ACCESSION AX592373
VERSION AX592373.1 GI:27950475
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 63 04-JUL-2002;
Dynavax Technologies Corporation (US)
FEATURES Location/Qualifiers
source 1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
ORIGIN

Query Match 100.0%; Score 8; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 3 AACGTTCG 10

RESULT 5
AX592374
LOCUS AX592374 10 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 64 from Patent WO02052002.
ACCESSION AX592374
VERSION AX592374.1 GI:27950476
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 64 04-JUL-2002;
Dynavax Technologies Corporation (US)
FEATURES Location/Qualifiers
source 1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
ORIGIN

Query Match 100.0%; Score 8; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 3 AACGTTCG 10

```
RESULT 6
AX592377
LOCUS       AX592377                10 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 67 from Patent WO02052002.
ACCESSION   AX592377
VERSION     AX592377.1  GI:27950479
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 67 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match           100.0%;  Score 8;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 7
AX592382
LOCUS       AX592382                10 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 72 from Patent WO02052002.
ACCESSION   AX592382
VERSION     AX592382.1  GI:27950484
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 72 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match           100.0%;  Score 8;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 8
AX592387
LOCUS       AX592387                10 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 77 from Patent WO02052002.
ACCESSION   AX592387
VERSION     AX592387.1  GI:27950489
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 77 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match           100.0%;  Score 8;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 9
AX592387/c
LOCUS       AX592387                10 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 77 from Patent WO02052002.
ACCESSION   AX592387
VERSION     AX592387.1  GI:27950489
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 77 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match           100.0%;  Score 8;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 10
AX592389
LOCUS       AX592389                10 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 79 from Patent WO02052002.
ACCESSION   AX592389
VERSION     AX592389.1  GI:27950491
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 79 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
     misc_feature    1
                     /note="n = 5-bromocytosine"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 11
AX592390
LOCUS       AX592390                  10 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 80 from Patent WO02052002.
ACCESSION   AX592390
VERSION     AX592390.1  GI:27950492
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 80 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 12
AX592391
LOCUS       AX592391                  10 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 81 from Patent WO02052002.
ACCESSION   AX592391
VERSION     AX592391.1  GI:27950493
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 81 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 13
AX592392
LOCUS       AX592392                  10 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 82 from Patent WO02052002.
ACCESSION   AX592392
VERSION     AX592392.1  GI:27950494
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 82 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 14
AX592412
LOCUS       AX592412                  11 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 102 from Patent WO02052002.
ACCESSION   AX592412
VERSION     AX592412.1  GI:27950514
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 102 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          4 AACGTTCG 11


RESULT 15
AX592412/c
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LOCUS       AX592412                 11 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 102 from Patent WO02052002.
ACCESSION   AX592412
VERSION     AX592412.1  GI:27950514
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 102 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          9 AACGTTCG 2


RESULT 16
AX592424
LOCUS       AX592424                 11 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 114 from Patent WO02052002.
ACCESSION   AX592424
VERSION     AX592424.1  GI:27950526
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 114 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
     misc_feature    2
                     /note="n = 5-bromocytosine"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          4 AACGTTCG 11


RESULT 17
AR176675
LOCUS       AR176675                 12 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 6 from patent US 6312894.
ACCESSION   AR176675
VERSION     AR176675.1  GI:17919030
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Hedgpeth,J., Afonina,I.A., Kutyavin,I.V., Lukhtanov,E.A.,
            Belousov,E.S. and Meyer,R.B. Jr.
  TITLE     Hybridization and mismatch discrimination using oligonucleotides
            conjugated to minor groove binders
  JOURNAL   Patent: US 6312894-A 6 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12


RESULT 18
BD260026
LOCUS       BD260026                 12 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Hybridization and mismatch discrimination using oligonucleotides
            conjugated to minor groove binders.
ACCESSION   BD260026
VERSION     BD260026.1  GI:33069796
KEYWORDS    JP 2002527040-A/6.
SOURCE      Escherichia coli
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Hedgpeth,J., Afonina,I.A., Kutyavin,I.V., Lukhtanov,E.A.,
            Belousov,E.S. and Jr,R.B.M.
  TITLE     Hybridization and mismatch discrimination using oligonucleotides
            conjugated to minor groove binders
  JOURNAL   Patent: JP 2002527040-A 6 27-AUG-2002;
            EPOCH BIOSCIENCES INC
COMMENT     OS   Escherichia coli
            PN   JP 2002527040-A/6
            PD   27-AUG-2002
            PF   05-APR-1999 JP 2000542342
            PR   03-APR-1998 US    09/054832
            PI   JOEL HEDGPETH,IRINA A AFONINA,IGOR V KUTYAVIN,EUGENY A  PI
            LUKHTANOV,
            PI   EVGENIY S BELOUSOV,RICH B MEYER JR
            PC   C12N15/09,C12N15/09,C07H21/02,C07H21/04,C12Q1/68,G01N21/78, PC
              G01N33/483,
            PC   G01N33/53,G01N33/566,C12N15/00,C12N15/00
            CC   Hybridization and mismatch discrimination using  CC
            oligonucleotides
            CC   conjugated to minor groove binders
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Escherichia coli'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Escherichia coli"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:562"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12
```

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RESULT 19
AR437498/c
LOCUS       AR437498                  12 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 42 from patent US 6660475.
ACCESSION   AR437498
VERSION     AR437498.1  GI:40202572
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Jack,W.E., Schildkraut,I. and Menin,J.F.
  TITLE     Use of site-specific nicking endonucleases to create
            single-stranded regions and applications thereof
  JOURNAL   Patent: US 6660475-A 42 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         11 AACGTTCG 4


RESULT 20
AX592417
LOCUS       AX592417                  12 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 107 from Patent WO02052002.
ACCESSION   AX592417
VERSION     AX592417.1  GI:27950519
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 107 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12


RESULT 21
AX592419
LOCUS       AX592419                  12 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 109 from Patent WO02052002.
ACCESSION   AX592419
VERSION     AX592419.1  GI:27950521
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 109 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12


RESULT 22
AX592407
LOCUS       AX592407                  13 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 97 from Patent WO02052002.
ACCESSION   AX592407
VERSION     AX592407.1  GI:27950509
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 97 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          6 AACGTTCG 13


RESULT 23
AX592407/c
LOCUS       AX592407                  13 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 97 from Patent WO02052002.
ACCESSION   AX592407
VERSION     AX592407.1  GI:27950509
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 97 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match           100.0%;  Score 8;  DB 6;  Length 13;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         11 AACGTTCG 4


RESULT 24
AX592409
LOCUS       AX592409                 13 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 99 from Patent WO02052002.
ACCESSION   AX592409
VERSION     AX592409.1  GI:27950511
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 99 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
     misc_feature    2
                     /note="n = 5-bromocytosine"
ORIGIN

  Query Match           100.0%;  Score 8;  DB 6;  Length 13;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          6 AACGTTCG 13


RESULT 25
AX592409/c
LOCUS       AX592409                 13 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 99 from Patent WO02052002.
ACCESSION   AX592409
VERSION     AX592409.1  GI:27950511
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 99 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
     misc_feature    2
                     /note="n = 5-bromocytosine"
ORIGIN

  Query Match           100.0%;  Score 8;  DB 6;  Length 13;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         11 AACGTTCG 4


RESULT 26
AX592411
LOCUS       AX592411                 13 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 101 from Patent WO02052002.
ACCESSION   AX592411
VERSION     AX592411.1  GI:27950513
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 101 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match           100.0%;  Score 8;  DB 6;  Length 13;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          6 AACGTTCG 13


RESULT 27
AX592413
LOCUS       AX592413                 13 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 103 from Patent WO02052002.
ACCESSION   AX592413
VERSION     AX592413.1  GI:27950515
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 103 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match           100.0%;  Score 8;  DB 6;  Length 13;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          6 AACGTTCG 13


RESULT 28
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AX592422
LOCUS       AX592422                 13 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 112 from Patent WO02052002.
ACCESSION   AX592422
VERSION     AX592422.1  GI:27950524
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 112 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
     misc_feature    2
                     /note="n = 5-bromocytosine"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          6 AACGTTCG 13


RESULT 29
AR148617
LOCUS       AR148617                 14 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 11 from patent US 6225292.
ACCESSION   AR148617
VERSION     AR148617.1  GI:15112707
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Raz,E. and Roman,M.
  TITLE     Inhibitors of DNA immunostimulatory sequence activity
  JOURNAL   Patent: US 6225292-A 11 01-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          6 AACGTTCG 13


RESULT 30
AX592408
LOCUS       AX592408                 14 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 98 from Patent WO02052002.
ACCESSION   AX592408
VERSION     AX592408.1  GI:27950510
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 98 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          7 AACGTTCG 14


RESULT 31
AX592408/c
LOCUS       AX592408                 14 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 98 from Patent WO02052002.
ACCESSION   AX592408
VERSION     AX592408.1  GI:27950510
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 98 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         12 AACGTTCG 5


RESULT 32
AX592410
LOCUS       AX592410                 14 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 100 from Patent WO02052002.
ACCESSION   AX592410
VERSION     AX592410.1  GI:27950512
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 100 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
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     misc_feature    2
                     /note="n = 5-bromocytosine"
     misc_feature    5
                     /note="n = 5-bromocytosine"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          7 AACGTTCG 14


RESULT 33
AX592425
LOCUS       AX592425                  14 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 115 from Patent WO02052002.
ACCESSION   AX592425
VERSION     AX592425.1  GI:27950527
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 115 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
     misc_feature    2
                     /note="n = 5-bromocytosine"
     misc_feature    5
                     /note="n = 5-bromocytosine"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          7 AACGTTCG 14


RESULT 34
AX592428
LOCUS       AX592428                  14 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 118 from Patent WO02052002.
ACCESSION   AX592428
VERSION     AX592428.1  GI:27950530
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 118 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
     misc_feature    5
                     /note="n = 5-bromocytosine"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          7 AACGTTCG 14


RESULT 35
BD136184
LOCUS       BD136184                  14 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Inhibitors of DNA immunostimulatory sequence activity.
ACCESSION   BD136184
VERSION     BD136184.1  GI:23231129
KEYWORDS    JP 2002505580-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Raz,E. and Roman,M.
  TITLE     Inhibitors of DNA immunostimulatory sequence activity
  JOURNAL   Patent: JP 2002505580-A 11 19-FEB-2002;
            DYNAVAX TECHNOLOGIES CORP, THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA
COMMENT     OS   Artificial Sequence
            PN   JP 2002505580-A/11
            PD   19-FEB-2002
            PF   05-JUN-1998 JP 1999502803
            PR   06-JUN-1997 US    60/048793
            PI   EYAL RAZ,MARK ROMAN
            PC   C12N15/00,C12N15/63,C12N15/79,C12N15/09,A61K48/00 CC
            Oligonucleotide
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          6 AACGTTCG 13


RESULT 36
AX592418
LOCUS       AX592418                  15 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 108 from Patent WO02052002.
ACCESSION   AX592418
VERSION     AX592418.1  GI:27950520
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 108 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 15


RESULT 37
AX663401/c
LOCUS       AX663401                 15 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 27 from Patent WO02097126.
ACCESSION   AX663401
VERSION     AX663401.1  GI:29163741
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weizenegger,M.
  TITLE     Method for detecting gram-positive bacteria
  JOURNAL   Patent: WO 02097126-A 27 05-DEC-2002;
            Hain Lifeschience GmbH (DE)
FEATURES             Location/Qualifiers
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                     /note="Sonde"
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         11 AACGTTCG 4


RESULT 38
AR176673
LOCUS       AR176673                 16 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 4 from patent US 6312894.
ACCESSION   AR176673
VERSION     AR176673.1  GI:17919028
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Hedgpeth,J., Afonina,I.A., Kutyavin,I.V., Lukhtanov,E.A.,
            Belousov,E.S. and Meyer,R.B. Jr.
  TITLE     Hybridization and mismatch discrimination using oligonucleotides
            conjugated to minor groove binders
  JOURNAL   Patent: US 6312894-A 4 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           100.0%;  Score 8;  DB 6;  Length 16;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12


RESULT 39
BD260024
LOCUS       BD260024                 16 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Hybridization and mismatch discrimination using oligonucleotides
            conjugated to minor groove binders.
ACCESSION   BD260024
VERSION     BD260024.1  GI:33069794
KEYWORDS    JP 2002527040-A/4.
SOURCE      Escherichia coli
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Hedgpeth,J., Afonina,I.A., Kutyavin,I.V., Lukhtanov,E.A.,
            Belousov,E.S. and Jr,R.B.M.
  TITLE     Hybridization and mismatch discrimination using oligonucleotides
            conjugated to minor groove binders
  JOURNAL   Patent: JP 2002527040-A 4 27-AUG-2002;
            EPOCH BIOSCIENCES INC
COMMENT     OS   Escherichia coli
            PN   JP 2002527040-A/4
            PD   27-AUG-2002
            PF   05-APR-1999 JP 2000542342
            PR   03-APR-1998 US    09/054832
            PI   JOEL HEDGPETH,IRINA A AFONINA,IGOR V KUTYAVIN,EUGENY A  PI
            LUKHTANOV,
            PI   EVGENIY S BELOUSOV,RICH B MEYER JR
            PC   C12N15/09,C12N15/09,C07H21/02,C07H21/04,C12Q1/68,G01N21/78, PC
              G01N33/483,
            PC   G01N33/53,G01N33/566,C12N15/00,C12N15/00
            CC   Hybridization and mismatch discrimination using  CC
            oligonucleotides
            CC   conjugated to minor groove binders
            FH   Key             Location/Qualifiers
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            FT                   /organism='Escherichia coli'.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           100.0%;  Score 8;  DB 6;  Length 16;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12


RESULT 40
AX194461
LOCUS       AX194461                 16 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 61 from Patent WO0151500.
ACCESSION   AX194461
VERSION     AX194461.1  GI:15385117
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 61 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          6 AACGTTCG 13


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Perfect score: 8
Sequence: 1 aacgttcg 8

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseqn2003cs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	8	100.0	8	8	ACD99956	Acd99956 Immunosti
	3	8	100.0	10	5	AAF34842	Aaf34842 Yeast NOR
	4	8	100.0	10	6	ABQ75130	Abq75130 ISS immun
	5	8	100.0	10	6	ABQ75136	Abq75136 ISS immun
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	8	8	100.0	10	6	ABQ75148	Abq75148 ISS immun
	9	8	100.0	10	6	ABQ75149	Abq75149 ISS immun
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	12	8	100.0	10	6	ABQ75131	Abq75131 ISS immun
	13	8	100.0	10	6	ABQ75151	Abq75151 ISS immun
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	15	8	100.0	10	8	ADB88804	Adb88804 Chimeric
	16	8	100.0	10	8	ADB88818	Adb88818 Chimeric
	17	8	100.0	10	8	ADB88816	Adb88816 Chimeric
	18	8	100.0	10	8	ADB88802	Adb88802 Chimeric
	19	8	100.0	10	8	ADB88819	Adb88819 Chimeric
	20	8	100.0	10	8	ADB88814	Adb88814 Chimeric
c	21	8	100.0	10	8	ADB88814	Adb88814 Chimeric
	22	8	100.0	10	8	ADB88803	Adb88803 Chimeric
	23	8	100.0	10	8	ADB88809	Adb88809 Chimeric
	24	8	100.0	10	8	ADB88817	Adb88817 Chimeric
	25	8	100.0	11	6	ABQ75229	Abq75229 ISS immun
c	26	8	100.0	11	6	ABQ75229	Abq75229 ISS immun
	27	8	100.0	11	6	ABQ75242	Abq75242 ISS immun
	28	8	100.0	11	8	ADB88900	Adb88900 Chimeric
c	29	8	100.0	11	8	ADB88900	Adb88900 Chimeric
	30	8	100.0	11	8	ADB88915	Adb88915 Chimeric
	31	8	100.0	12	2	AAZ32399	Aaz32399 M13mp19 g
c	32	8	100.0	12	5	ABI33516	Abi33516 Oligonucl
	33	8	100.0	12	6	ABQ75234	Abq75234 ISS immun
	34	8	100.0	12	6	ABQ75236	Abq75236 ISS immun
c	35	8	100.0	12	7	ACA74455	Aca74455 Generated
	36	8	100.0	12	8	ADB88908	Adb88908 Chimeric
	37	8	100.0	12	8	ADB88906	Adb88906 Chimeric
	38	8	100.0	13	1	AAN70417	Aan70417 Oligonucl
c	39	8	100.0	13	5	ABH35805	Abh35805 Oligonucl
c	40	8	100.0	13	5	ABH14166	Abh14166 Oligonucl
c	41	8	100.0	13	5	ABF27402	Abf27402 Oligonucl
c	42	8	100.0	13	5	ABH11809	Abh11809 Oligonucl
c	43	8	100.0	13	5	ABH58135	Abh58135 Oligonucl
	44	8	100.0	13	5	ABF27026	Abf27026 Oligonucl
	45	8	100.0	13	5	ABH11808	Abh11808 Oligonucl

ALIGNMENTS

RESULT 1
ABS78185/c
ID ABS78185 standard; DNA; 8 BP.
XX
AC ABS78185;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #669.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 31; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,

```
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 6;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.3e+08;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 2
ACD99956/c
ID   ACD99956 standard; DNA; 8 BP.
XX
AC   ACD99956;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #642.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 26; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 8;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.3e+08;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 3
AAF34842
ID   AAF34842 standard; DNA; 10 BP.
XX
AC   AAF34842;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1581.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 56; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 5;  Length 10;
```

Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AACGTTCG 8
              ||||||||
Db          1 AACGTTCG 8
```

RESULT 4
ABQ75130
ID ABQ75130 standard; DNA; 10 BP.
XX
AC ABQ75130;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:63.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Disclosure; Page 5; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide which is
CC specifically not claimed in the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 8; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10
```

RESULT 5
ABQ75136
ID ABQ75136 standard; DNA; 10 BP.
XX
AC ABQ75136;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:77.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Claim 3; Page 88; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide which is
CC specifically claimed in the present invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 8; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10
```

RESULT 6
ABQ75136/c
ID ABQ75136 standard; DNA; 10 BP.
XX
AC ABQ75136;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:77.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Claim 3; Page 88; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide which is
CC specifically claimed in the present invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 8;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1
```

RESULT 7
ABQ75150
ID ABQ75150 standard; DNA; 10 BP.
XX
AC ABQ75150;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:81.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT misc_RNA   1
FT   /*tag= a
FT   /note= "uracil"
FT misc_RNA   7
FT   /*tag= b
FT   /note= "uracil"
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Claim 2; Page 88; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide which is
CC specifically claimed in the present invention

```
XX
SQ   Sequence 10 BP; 2 A; 2 C; 2 G; 2 T; 2 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 6;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 2.6e+04;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||:|||
Db          3 AACGUTCG 10


RESULT 8
ABQ75148
ID   ABQ75148 standard; DNA; 10 BP.
XX
AC   ABQ75148;
XX
DT   05-NOV-2002  (first entry)
XX
DE   ISS immunomodulatory oligonucleotide SEQ ID NO:79.
XX
KW   Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW   allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW   idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW   malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW   immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW   virucide; antibacterial; protozoacide; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-bromocytosine"
XX
PN   WO200252002-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-US050821.
XX
PR   27-DEC-2000; 2000US-0258675P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D;
XX
DR   WPI; 2002-657426/70.
XX
PT   Immunomodulatory polynucleotide for modulating an immune response in a
PT   subject suffering from disorders associated with Th2-type immune
PT   response, e.g. allergy, or infectious disease, comprises an
PT   immunostimulatory sequence.
XX
PS   Claim 2; Page 88; 95pp; English.
XX
CC   The present invention describes an immunomodulatory polynucleotide (I)
CC   comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC   immunomodulatory composition comprising (I); (2) an immunomodulatory
CC   polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC   biodegradable MC, where the MC is less than 10 micrometre in size; and
CC   (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC   antibacterial and protozoacide activities, and can be used as a modulator
CC   of immune response. (I) is useful for modulating an immune response in an
CC   individual suffering from disorders associated with a Th2-type immune
CC   response, especially an allergy or asthma, or an infectious disease. (I)
CC   is also useful for increasing interferon-gamma (IFN-gamma) in an
CC   individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC   individual having a viral infection. (I) is further useful for
CC   ameliorating a symptom of an infectious disease caused by a cellular
CC   pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC   toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC   symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC   allergy-related disorder, in particular asthma in an individual. The
CC   present sequence represents an immunomodulatory oligonucleotide which is
CC   specifically claimed in the present invention
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 2 T; 0 U; 1 Other;

  Query Match             100.0%;  Score 8;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 9
ABQ75149
ID   ABQ75149 standard; DNA; 10 BP.
XX
AC   ABQ75149;
XX
DT   05-NOV-2002  (first entry)
XX
DE   ISS immunomodulatory oligonucleotide SEQ ID NO:80.
XX
KW   Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW   allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW   idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW   malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW   immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW   virucide; antibacterial; protozoacide; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        7
FT                   /*tag=  a
FT                   /note= "uracil"
XX
PN   WO200252002-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-US050821.
XX
PR   27-DEC-2000; 2000US-0258675P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D;
XX
DR   WPI; 2002-657426/70.
XX
PT   Immunomodulatory polynucleotide for modulating an immune response in a
PT   subject suffering from disorders associated with Th2-type immune
PT   response, e.g. allergy, or infectious disease, comprises an
PT   immunostimulatory sequence.
XX
PS   Claim 2; Page 88; 95pp; English.
XX
CC   The present invention describes an immunomodulatory polynucleotide (I)
CC   comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC   immunomodulatory composition comprising (I); (2) an immunomodulatory
CC   polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC   biodegradable MC, where the MC is less than 10 micrometre in size; and
CC   (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC   antibacterial and protozoacide activities, and can be used as a modulator
CC   of immune response. (I) is useful for modulating an immune response in an
CC   individual suffering from disorders associated with a Th2-type immune
CC   response, especially an allergy or asthma, or an infectious disease. (I)
CC   is also useful for increasing interferon-gamma (IFN-gamma) in an
```

CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide which is
CC specifically claimed in the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 2 G; 3 T; 1 U; 0 Other;

Query Match 100.0%; Score 8; DB 6; Length 10;
Best Local Similarity 87.5%; Pred. No. 2.6e+04;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||:|||
Db 3 AACGUTCG 10

RESULT 10
ABQ75134
ID ABQ75134 standard; DNA; 10 BP.
XX
AC ABQ75134;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:67.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 7
FT /*tag= a
FT /note= "uracil"
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Claim 3; Page 88; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide which is
CC specifically claimed in the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 3 G; 2 T; 1 U; 0 Other;

Query Match 100.0%; Score 8; DB 6; Length 10;
Best Local Similarity 87.5%; Pred. No. 2.6e+04;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||:|||
Db 3 AACGUTCG 10

RESULT 11
ABQ75143
ID ABQ75143 standard; DNA; 10 BP.
XX
AC ABQ75143;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:72.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Claim 2; Page 88; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an

CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide which is
CC specifically claimed in the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 8; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 3 AACGTTCG 10

RESULT 12
ABQ75131
ID ABQ75131 standard; DNA; 10 BP.
XX
AC ABQ75131;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:64.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Disclosure; Page 5; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide which is
CC specifically not claimed in the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 8; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 3 AACGTTCG 10

RESULT 13
ABQ75151
ID ABQ75151 standard; DNA; 10 BP.
XX
AC ABQ75151;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:82.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Claim 2; Page 88; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)

```
CC   is also useful for increasing interferon-gamma (IFN-gamma) in an
CC   individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC   individual having a viral infection. (I) is further useful for
CC   ameliorating a symptom of an infectious disease caused by a cellular
CC   pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC   toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC   symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC   allergy-related disorder, in particular asthma in an individual. The
CC   present sequence represents an immunomodulatory oligonucleotide which is
CC   specifically claimed in the present invention
XX
SQ   Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 14
ABN88794
ID   ABN88794 standard; DNA; 10 BP.
XX
AC   ABN88794;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Exemplary oligonucleotide sequence #3.
XX
KW   Nucleic acid sequencing; diagnosis; mutation; fluorescence; detection;
KW   labeling; ss.
XX
OS   Synthetic.
XX
PN   JP2002055080-A.
XX
PD   20-FEB-2002.
XX
PF   08-AUG-2000; 2000JP-00245516.
XX
PR   08-AUG-2000; 2000JP-00245516.
XX
PA   (HITA ) HITACHI LTD.
XX
DR   WPI; 2002-465655/50.
XX
PT   Nucleic acid sequencer comprises units for fluorescently labeling nucleic
PT   acid fragments, generating fluorescence intensity waveform data and
PT   correlating the data to base sequence of the nucleic acid.
XX
PS   Disclosure; Fig 2; 11pp; Japanese.
XX
CC   The present invention describes a nucleic acid sequencer having units for
CC   preparing nucleic acid fragments; labeling them with fluorescent labels;
CC   detecting fluorescence intensity waveform data; and correlating the data
CC   to the base sequence of the nucleic acid. The base sequence is determined
CC   by comparing the fluorescence data with several stored reference
CC   fluorescence intensity waveform data obtained from samples whose base
CC   sequences are known. The nucleic acid sequencer can be used for
CC   determining base sequences automatically. The apparatus is useful for
CC   detecting mutations in gene sequence for diagnosis and determining
CC   disease susceptibility. The nucleic acid base sequences are determined
CC   accurately. The present sequence represents an exemplary oligonucleotide
CC   base sequence, which is used in the exemplification of the present
CC   invention
XX
SQ   Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          1 AACGTTCG 8


RESULT 15
ADB88804
ID   ADB88804 standard; DNA; 10 BP.
XX
AC   ADB88804;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Chimeric immunomodulatory compound DNA sequence, SEQ ID No 7.
XX
KW   chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW   spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW   Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW   IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW   immunoglobulin E; IgE; allergy; cancer;
KW   stimulating cellular immune system cell; ss.
XX
OS   Synthetic.
XX
PN   WO2003000922-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US020025.
XX
PR   21-JUN-2001; 2001US-0299883P.
PR   23-APR-2002; 2002US-0375253P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D,  Tuck SF;
XX
DR   WPI; 2003-210159/20.
XX
PT   Novel chimeric immunomodulatory compound having immunomodulatory
PT   activity, useful for modulating an immune response and for treating
PT   cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS   Disclosure; Page 32; 224pp; English.
XX
CC   The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC   having immunomodulatory activity, comprising two or more nucleic acid
CC   moieties and one or more non-nucleic acid spacer moieties, where at least
CC   one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC   acid moieties, where the spacer is not a polypeptide, and at least one
CC   nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC   immunomodulatory compounds more specifically contain the nucleic acid
CC   spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC   CIC's are useful for modulating an immune response in an individual,
CC   where the individual suffers from a disorder associated with a Th2-type
CC   immune response which is an allergy or allergy-induced asthma, and an
CC   infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC   alpha; in an individual, where the individual has idiopathic pulmonary
CC   fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC   symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC   disorder in an individual, where the IgE-related disorder is allergy, or
CC   an allergy-related disorder. CIC's are also useful for treating cancer
CC   and can be used for stimulating cellular immune system cells production
CC   in an individual. This polynucleotide sequence represents a DNA sequence
CC   which is a nucleic acid moiety part of a chimeric immunomodulatory compound
CC   of the invention.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 2 T; 1 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 8;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 2.6e+04;
```

```
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||:|||
Db          3 AACGUTCG 10


RESULT 16
ADB88818
ID   ADB88818 standard; DNA; 10 BP.
XX
AC   ADB88818;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Chimeric immunomodulatory compound DNA sequence, SEQ ID No 21.
XX
KW   chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW   spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW   Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW   IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW   immunoglobulin E; IgE; allergy; cancer;
KW   stimulating cellular immune system cell; ss.
XX
OS   Synthetic.
XX
PN   WO2003000922-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US020025.
XX
PR   21-JUN-2001; 2001US-0299883P.
PR   23-APR-2002; 2002US-0375253P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D,  Tuck SF;
XX
DR   WPI; 2003-210159/20.
XX
PT   Novel chimeric immunomodulatory compound having immunomodulatory
PT   activity, useful for modulating an immune response and for treating
PT   cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS   Disclosure; Page 33; 224pp; English.
XX
CC   The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC   having immunomodulatory activity, comprising two or more nucleic acid
CC   moieties and one or more non-nucleic acid spacer moieties, where at least
CC   one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC   acid moieties, where the spacer is not a polypeptide, and at least one
CC   nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC   immunodulatory compounds more specifically contain the nucleic acid
CC   spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC   CIC's are useful for modulating an immune response in an individual,
CC   where the individual suffers from a disorder associated with a Th2-type
CC   immune response which is an allergy or allergy-induced asthma, and an
CC   infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC   alpha; in an individual, where the individual has idiopathic pulmonary
CC   fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC   symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC   disorder in an individual, where the IgE-related disorder is allergy, or
CC   an allergy-related disorder. CIC's are also useful for treating cancer
CC   and can be used for stimulating cellular immune system cells production
CC   in an individual. This polynucleotide sequence represents a DNA sequence
CC   which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC   of the invention.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 2 G; 2 T; 2 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 8;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 2.6e+04;
```

```
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||:|||
Db          3 AACGUTCG 10


RESULT 17
ADB88816
ID   ADB88816 standard; DNA; 10 BP.
XX
AC   ADB88816;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Chimeric immunomodulatory compound DNA sequence, SEQ ID No 19.
XX
KW   chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW   spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW   Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW   IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW   immunoglobulin E; IgE; allergy; cancer;
KW   stimulating cellular immune system cell; ss.
XX
OS   Synthetic.
XX
PN   WO2003000922-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US020025.
XX
PR   21-JUN-2001; 2001US-0299883P.
PR   23-APR-2002; 2002US-0375253P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D,  Tuck SF;
XX
DR   WPI; 2003-210159/20.
XX
PT   Novel chimeric immunomodulatory compound having immunomodulatory
PT   activity, useful for modulating an immune response and for treating
PT   cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS   Disclosure; Page 33; 224pp; English.
XX
CC   The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC   having immunomodulatory activity, comprising two or more nucleic acid
CC   moieties and one or more non-nucleic acid spacer moieties, where at least
CC   one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC   acid moieties, where the spacer is not a polypeptide, and at least one
CC   nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC   immunodulatory compounds more specifically contain the nucleic acid
CC   spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC   CIC's are useful for modulating an immune response in an individual,
CC   where the individual suffers from a disorder associated with a Th2-type
CC   immune response which is an allergy or allergy-induced asthma, and an
CC   infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC   alpha; in an individual, where the individual has idiopathic pulmonary
CC   fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC   symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC   disorder in an individual, where the IgE-related disorder is allergy, or
CC   an allergy-related disorder. CIC's are also useful for treating cancer
CC   and can be used for stimulating cellular immune system cells production
CC   in an individual. This polynucleotide sequence represents a DNA sequence
CC   which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC   of the invention.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 2 T; 0 U; 1 Other;

  Query Match             100.0%;  Score 8;  DB 8;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
```

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10
```

RESULT 18
ADB88802
ID ADB88802 standard; DNA; 10 BP.
XX
AC ADB88802;
XX
DT 04-DEC-2003 (first entry)
XX
DE Chimeric immunomodulatory compound DNA sequence, SEQ ID No 5.
XX
KW chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW immunoglobulin E; IgE; allergy; cancer;
KW stimulating cellular immune system cell; ss.
XX
OS Synthetic.
XX
PN WO2003000922-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US020025.
XX
PR 21-JUN-2001; 2001US-0299883P.
PR 23-APR-2002; 2002US-0375253P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D, Tuck SF;
XX
DR WPI; 2003-210159/20.
XX
PT Novel chimeric immunomodulatory compound having immunomodulatory
PT activity, useful for modulating an immune response and for treating
PT cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS Disclosure; Page 32; 224pp; English.
XX
CC The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC having immunomodulatory activity, comprising two or more nucleic acid
CC moieties and one or more non-nucleic acid spacer moieties, where at least
CC one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC acid moieties, where the spacer is not a polypeptide, and at least one
CC nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC immunodulatory compounds more specifically contain the nucleic acid
CC spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC CIC's are useful for modulating an immune response in an individual,
CC where the individual suffers from a disorder associated with a Th2-type
CC immune response which is an allergy or allergy-induced asthma, and an
CC infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC alpha; in an individual, where the individual has idiopathic pulmonary
CC fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC disorder in an individual, where the IgE-related disorder is allergy, or
CC an allergy-related disorder. CIC's are also useful for treating cancer
CC and can be used for stimulating cellular immune system cells production
CC in an individual. This polynucleotide sequence represents a DNA sequence
CC which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC of the invention.
XX
SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 8; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10
```

RESULT 19
ADB88819
ID ADB88819 standard; DNA; 10 BP.
XX
AC ADB88819;
XX
DT 04-DEC-2003 (first entry)
XX
DE Chimeric immunomodulatory compound DNA sequence, SEQ ID No 22.
XX
KW chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW immunoglobulin E; IgE; allergy; cancer;
KW stimulating cellular immune system cell; ss.
XX
OS Synthetic.
XX
PN WO2003000922-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US020025.
XX
PR 21-JUN-2001; 2001US-0299883P.
PR 23-APR-2002; 2002US-0375253P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D, Tuck SF;
XX
DR WPI; 2003-210159/20.
XX
PT Novel chimeric immunomodulatory compound having immunomodulatory
PT activity, useful for modulating an immune response and for treating
PT cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS Disclosure; Page 33; 224pp; English.
XX
CC The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC having immunomodulatory activity, comprising two or more nucleic acid
CC moieties and one or more non-nucleic acid spacer moieties, where at least
CC one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC acid moieties, where the spacer is not a polypeptide, and at least one
CC nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC immunodulatory compounds more specifically contain the nucleic acid
CC spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC CIC's are useful for modulating an immune response in an individual,
CC where the individual suffers from a disorder associated with a Th2-type
CC immune response which is an allergy or allergy-induced asthma, and an
CC infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC alpha; in an individual, where the individual has idiopathic pulmonary
CC fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC disorder in an individual, where the IgE-related disorder is allergy, or
CC an allergy-related disorder. CIC's are also useful for treating cancer
CC and can be used for stimulating cellular immune system cells production
CC in an individual. This polynucleotide sequence represents a DNA sequence
CC which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC of the invention.
XX
SQ Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 8; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;

```
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 20
ADB88814
ID   ADB88814 standard; DNA; 10 BP.
XX
AC   ADB88814;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Chimeric immunomodulatory compound DNA sequence, SEQ ID No 17.
XX
KW   chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW   spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW   Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW   IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW   immunoglobulin E; IgE; allergy; cancer;
KW   stimulating cellular immune system cell; ss.
XX
OS   Synthetic.
XX
PN   WO2003000922-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US020025.
XX
PR   21-JUN-2001; 2001US-0299883P.
PR   23-APR-2002; 2002US-0375253P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D,  Tuck SF;
XX
DR   WPI; 2003-210159/20.
XX
PT   Novel chimeric immunomodulatory compound having immunomodulatory
PT   activity, useful for modulating an immune response and for treating
PT   cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS   Disclosure; Page 33; 224pp; English.
XX
CC   The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC   having immunomodulatory activity, comprising two or more nucleic acid
CC   moieties and one or more non-nucleic acid spacer moieties, where at least
CC   one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC   acid moieties, where the spacer is not a polypeptide, and at least one
CC   nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC   immunodulatory compounds more specifically contain the nucleic acid
CC   spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC   CIC's are useful for modulating an immune response in an individual,
CC   where the individual suffers from a disorder associated with a Th2-type
CC   immune response which is an allergy or allergy-induced asthma, and an
CC   infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC   alpha; in an individual, where the individual has idiopathic pulmonary
CC   fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC   symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC   disorder in an individual, where the IgE-related disorder is allergy, or
CC   an allergy-related disorder. CIC's are also useful for treating cancer
CC   and can be used for stimulating cellular immune system cells production
CC   in an individual. This polynucleotide sequence represents a DNA sequence
CC   which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC   of the invention.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 8;  DB 8;  Length 10;
  Best Local Similarity 100.0%;  Pred. No. 2.6e+04;
```

```
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 21
ADB88814/c
ID   ADB88814 standard; DNA; 10 BP.
XX
AC   ADB88814;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Chimeric immunomodulatory compound DNA sequence, SEQ ID No 17.
XX
KW   chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW   spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW   Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW   IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW   immunoglobulin E; IgE; allergy; cancer;
KW   stimulating cellular immune system cell; ss.
XX
OS   Synthetic.
XX
PN   WO2003000922-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US020025.
XX
PR   21-JUN-2001; 2001US-0299883P.
PR   23-APR-2002; 2002US-0375253P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D,  Tuck SF;
XX
DR   WPI; 2003-210159/20.
XX
PT   Novel chimeric immunomodulatory compound having immunomodulatory
PT   activity, useful for modulating an immune response and for treating
PT   cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS   Disclosure; Page 33; 224pp; English.
XX
CC   The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC   having immunomodulatory activity, comprising two or more nucleic acid
CC   moieties and one or more non-nucleic acid spacer moieties, where at least
CC   one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC   acid moieties, where the spacer is not a polypeptide, and at least one
CC   nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC   immunodulatory compounds more specifically contain the nucleic acid
CC   spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC   CIC's are useful for modulating an immune response in an individual,
CC   where the individual suffers from a disorder associated with a Th2-type
CC   immune response which is an allergy or allergy-induced asthma, and an
CC   infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC   alpha; in an individual, where the individual has idiopathic pulmonary
CC   fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC   symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC   disorder in an individual, where the IgE-related disorder is allergy, or
CC   an allergy-related disorder. CIC's are also useful for treating cancer
CC   and can be used for stimulating cellular immune system cells production
CC   in an individual. This polynucleotide sequence represents a DNA sequence
CC   which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC   of the invention.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 8;  DB 8;  Length 10;
  Best Local Similarity 100.0%;  Pred. No. 2.6e+04;
```

```
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 22
ADB88803
ID   ADB88803 standard; DNA; 10 BP.
XX
AC   ADB88803;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Chimeric immunomodulatory compound DNA sequence, SEQ ID No 6.
XX
KW   chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW   spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW   Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW   IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW   immunoglobulin E; IgE; allergy; cancer;
KW   stimulating cellular immune system cell; ss.
XX
OS   Synthetic.
XX
PN   WO2003000922-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US020025.
XX
PR   21-JUN-2001; 2001US-0299883P.
PR   23-APR-2002; 2002US-0375253P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D,  Tuck SF;
XX
DR   WPI; 2003-210159/20.
XX
PT   Novel chimeric immunomodulatory compound having immunomodulatory
PT   activity, useful for modulating an immune response and for treating
PT   cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS   Disclosure; Page 32; 224pp; English.
XX
CC   The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC   having immunomodulatory activity, comprising two or more nucleic acid
CC   moieties and one or more non-nucleic acid spacer moieties, where at least
CC   one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC   acid moieties, where the spacer is not a polypeptide, and at least one
CC   nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC   immunodulatory compounds more specifically contain the nucleic acid
CC   spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC   CIC's are useful for modulating an immune response in an individual,
CC   where the individual suffers from a disorder associated with a Th2-type
CC   immune response which is an allergy or allergy-induced asthma, and an
CC   infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC   alpha; in an individual, where the individual has idiopathic pulmonary
CC   fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC   symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC   disorder in an individual, where the IgE-related disorder is allergy, or
CC   an allergy-related disorder. CIC's are also useful for treating cancer
CC   and can be used for stimulating cellular immune system cells production
CC   in an individual. This polynucleotide sequence represents a DNA sequence
CC   which is a nucleic acid moiety part of a chimeric immunomodulatory compound
CC   of the invention.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 8;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
```

```
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 23
ADB88809
ID   ADB88809 standard; DNA; 10 BP.
XX
AC   ADB88809;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Chimeric immunomodulatory compound DNA sequence, SEQ ID No 12.
XX
KW   chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW   spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW   Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW   IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW   immunoglobulin E; IgE; allergy; cancer;
KW   stimulating cellular immune system cell; ss.
XX
OS   Synthetic.
XX
PN   WO2003000922-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US020025.
XX
PR   21-JUN-2001; 2001US-0299883P.
PR   23-APR-2002; 2002US-0375253P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D,  Tuck SF;
XX
DR   WPI; 2003-210159/20.
XX
PT   Novel chimeric immunomodulatory compound having immunomodulatory
PT   activity, useful for modulating an immune response and for treating
PT   cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS   Disclosure; Page 32; 224pp; English.
XX
CC   The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC   having immunomodulatory activity, comprising two or more nucleic acid
CC   moieties and one or more non-nucleic acid spacer moieties, where at least
CC   one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC   acid moieties, where the spacer is not a polypeptide, and at least one
CC   nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC   immunodulatory compounds more specifically contain the nucleic acid
CC   spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC   CIC's are useful for modulating an immune response in an individual,
CC   where the individual suffers from a disorder associated with a Th2-type
CC   immune response which is an allergy or allergy-induced asthma, and an
CC   infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC   alpha; in an individual, where the individual has idiopathic pulmonary
CC   fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC   symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC   disorder in an individual, where the IgE-related disorder is allergy, or
CC   an allergy-related disorder. CIC's are also useful for treating cancer
CC   and can be used for stimulating cellular immune system cells production
CC   in an individual. This polynucleotide sequence represents a DNA sequence
CC   which is a nucleic acid moiety part of a chimeric immunomodulatory compound
CC   of the invention.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 8;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
```

```
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 24
ADB88817
ID   ADB88817 standard; DNA; 10 BP.
XX
AC   ADB88817;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Chimeric immunomodulatory compound DNA sequence, SEQ ID No 20.
XX
KW   chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW   spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW   Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW   IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW   immunoglobulin E; IgE; allergy; cancer;
KW   stimulating cellular immune system cell; ss.
XX
OS   Synthetic.
XX
PN   WO2003000922-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US020025.
XX
PR   21-JUN-2001; 2001US-0299883P.
PR   23-APR-2002; 2002US-0375253P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D,  Tuck SF;
XX
DR   WPI; 2003-210159/20.
XX
PT   Novel chimeric immunomodulatory compound having immunomodulatory
PT   activity, useful for modulating an immune response and for treating
PT   cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS   Disclosure; Page 33; 224pp; English.
XX
CC   The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC   having immunomodulatory activity, comprising two or more nucleic acid
CC   moieties and one or more non-nucleic acid spacer moieties, where at least
CC   one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC   acid moieties, where the spacer is not a polypeptide, and at least one
CC   nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC   immunodulatory compounds more specifically contain the nucleic acid
CC   spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC   CIC's are useful for modulating an immune response in an individual,
CC   where the individual suffers from a disorder associated with a Th2-type
CC   immune response which is an allergy or allergy-induced asthma, and an
CC   infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC   alpha; in an individual, where the individual has idiopathic pulmonary
CC   fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC   symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC   disorder in an individual, where the IgE-related disorder is allergy, or
CC   an allergy-related disorder. CIC's are also useful for treating cancer
CC   and can be used for stimulating cellular immune system cells production
CC   in an individual. This polynucleotide sequence represents a DNA sequence
CC   which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC   of the invention.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 2 G; 3 T; 1 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 8;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 2.6e+04;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||:|||
Db          3 AACGUTCG 10


RESULT 25
ABQ75229
ID   ABQ75229 standard; DNA; 11 BP.
XX
AC   ABQ75229;
XX
DT   05-NOV-2002  (first entry)
XX
DE   ISS immunomodulatory oligonucleotide SEQ ID NO:102.
XX
KW   Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW   allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW   idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW   malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW   immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW   virucide; antibacterial; protozoacide; ss.
XX
OS   Synthetic.
XX
PN   WO200252002-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-US050821.
XX
PR   27-DEC-2000; 2000US-0258675P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D;
XX
DR   WPI; 2002-657426/70.
XX
PT   Immunomodulatory polynucleotide for modulating an immune response in a
PT   subject suffering from disorders associated with Th2-type immune
PT   response, e.g. allergy, or infectious disease, comprises an
PT   immunostimulatory sequence.
XX
PS   Disclosure; Page 24; 95pp; English.
XX
CC   The present invention describes an immunomodulatory polynucleotide (I)
CC   comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC   immunomodulatory composition comprising (I); (2) an immunomodulatory
CC   polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC   biodegradable MC, where the MC is less than 10 micrometre in size; and
CC   (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC   antibacterial and protozoacide activities, and can be used as a modulator
CC   of immune response. (I) is useful for modulating an immune response in an
CC   individual suffering from disorders associated with a Th2-type immune
CC   response, especially an allergy or asthma, or an infectious disease. (I)
CC   is also useful for increasing interferon-gamma (IFN-gamma) in an
CC   individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC   individual having a viral infection. (I) is further useful for
CC   ameliorating a symptom of an infectious disease caused by a cellular
CC   pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC   toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC   symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC   allergy-related disorder, in particular asthma in an individual. The
CC   present sequence represents an immunomodulatory oligonucleotide from the
CC   present invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 AACGTTCG 8
              ||||||||
Db          4 AACGTTCG 11
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RESULT 26
ABQ75229/c
ID ABQ75229 standard; DNA; 11 BP.
XX
AC ABQ75229;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:102.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Disclosure; Page 24; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from the
CC present invention
XX
SQ Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

```
  Query Match           100.0%;  Score 8;  DB 6;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 AACGTTCG 8
              ||||||||
Db          9 AACGTTCG 2
```

RESULT 27
ABQ75242
ID ABQ75242 standard; DNA; 11 BP.
XX
AC ABQ75242;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:114.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT modified_base   2
FT   /*tag= a
FT   /mod_base= OTHER
FT   /note= "5-bromocytosine"
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Disclosure; Page 25; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from the
CC present invention
XX
SQ Sequence 11 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 1 Other;

```
  Query Match             100.0%;  Score 8;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          4 AACGTTCG 11


RESULT 28
ADB88900
ID   ADB88900 standard; DNA; 11 BP.
XX
AC   ADB88900;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Chimeric immunomodulatory compound DNA sequence, SEQ ID No 103.
XX
KW   chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW   spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW   Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW   IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW   immunoglobulin E; IgE; allergy; cancer;
KW   stimulating cellular immune system cell; ss.
XX
OS   Synthetic.
XX
PN   WO2003000922-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US020025.
XX
PR   21-JUN-2001; 2001US-0299883P.
PR   23-APR-2002; 2002US-0375253P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D,  Tuck SF;
XX
DR   WPI; 2003-210159/20.
XX
PT   Novel chimeric immunomodulatory compound having immunomodulatory
PT   activity, useful for modulating an immune response and for treating
PT   cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS   Disclosure; Page 36; 224pp; English.
XX
CC   The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC   having immunomodulatory activity, comprising two or more nucleic acid
CC   moieties and one or more non-nucleic acid spacer moieties, where at least
CC   one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC   acid moieties, where the spacer is not a polypeptide, and at least one
CC   nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC   immunodulatory compounds more specifically contain the nucleic acid
CC   spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC   CIC's are useful for modulating an immune response in an individual,
CC   where the individual suffers from a disorder associated with a Th2-type
CC   immune response which is an allergy or allergy-induced asthma, and an
CC   infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC   alpha; in an individual, where the individual has idiopathic pulmonary
CC   fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC   symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC   disorder in an individual, where the IgE-related disorder is allergy, or
CC   an allergy-related disorder. CIC's are also useful for treating cancer
CC   and can be used for stimulating cellular immune system cells production
CC   in an individual. This polynucleotide sequence represents a DNA sequence
CC   which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC   of the invention.
XX
SQ   Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
```

```
  Query Match             100.0%;  Score 8;  DB 8;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          4 AACGTTCG 11


RESULT 29
ADB88900/c
ID   ADB88900 standard; DNA; 11 BP.
XX
AC   ADB88900;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Chimeric immunomodulatory compound DNA sequence, SEQ ID No 103.
XX
KW   chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW   spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW   Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW   IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW   immunoglobulin E; IgE; allergy; cancer;
KW   stimulating cellular immune system cell; ss.
XX
OS   Synthetic.
XX
PN   WO2003000922-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US020025.
XX
PR   21-JUN-2001; 2001US-0299883P.
PR   23-APR-2002; 2002US-0375253P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D,  Tuck SF;
XX
DR   WPI; 2003-210159/20.
XX
PT   Novel chimeric immunomodulatory compound having immunomodulatory
PT   activity, useful for modulating an immune response and for treating
PT   cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS   Disclosure; Page 36; 224pp; English.
XX
CC   The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC   having immunomodulatory activity, comprising two or more nucleic acid
CC   moieties and one or more non-nucleic acid spacer moieties, where at least
CC   one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC   acid moieties, where the spacer is not a polypeptide, and at least one
CC   nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC   immunodulatory compounds more specifically contain the nucleic acid
CC   spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC   CIC's are useful for modulating an immune response in an individual,
CC   where the individual suffers from a disorder associated with a Th2-type
CC   immune response which is an allergy or allergy-induced asthma, and an
CC   infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC   alpha; in an individual, where the individual has idiopathic pulmonary
CC   fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC   symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC   disorder in an individual, where the IgE-related disorder is allergy, or
CC   an allergy-related disorder. CIC's are also useful for treating cancer
CC   and can be used for stimulating cellular immune system cells production
CC   in an individual. This polynucleotide sequence represents a DNA sequence
CC   which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC   of the invention.
XX
SQ   Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
```

Query Match 100.0%; Score 8; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
Db 9 AACGTTCG 2

RESULT 30
ADB88915
ID ADB88915 standard; DNA; 11 BP.
XX
AC ADB88915;
XX
DT 04-DEC-2003 (first entry)
XX
DE Chimeric immunomodulatory compound DNA sequence, SEQ ID No 118.
XX
KW chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW immunoglobulin E; IgE; allergy; cancer;
KW stimulating cellular immune system cell; ss.
XX
OS Synthetic.
XX
PN WO2003000922-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US020025.
XX
PR 21-JUN-2001; 2001US-0299883P.
PR 23-APR-2002; 2002US-0375253P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D, Tuck SF;
XX
DR WPI; 2003-210159/20.
XX
PT Novel chimeric immunomodulatory compound having immunomodulatory
PT activity, useful for modulating an immune response and for treating
PT cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS Disclosure; Page 36; 224pp; English.
XX
CC The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC having immunomodulatory activity, comprising two or more nucleic acid
CC moieties and one or more non-nucleic acid spacer moieties, where at least
CC one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC acid moieties, where the spacer is not a polypeptide, and at least one
CC nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC immunodulatory compounds more specifically contain the nucleic acid
CC spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC CIC's are useful for modulating an immune response in an individual,
CC where the individual suffers from a disorder associated with a Th2-type
CC immune response which is an allergy or allergy-induced asthma, and an
CC infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC alpha; in an individual, where the individual has idiopathic pulmonary
CC fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC disorder in an individual, where the IgE-related disorder is allergy, or
CC an allergy-related disorder. CIC's are also useful for treating cancer
CC and can be used for stimulating cellular immune system cells production
CC in an individual. This polynucleotide sequence represents a DNA sequence
CC which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC of the invention.
XX
SQ Sequence 11 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 1 Other;

Query Match 100.0%; Score 8; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
Db 4 AACGTTCG 11

RESULT 31
AAZ32399
ID AAZ32399 standard; DNA; 12 BP.
XX
AC AAZ32399;
XX
DT 26-JAN-2000 (first entry)
XX
DE M13mp19 genome oligonucleotide SEQ ID NO:6.
XX
KW M13mp19; MGB; minor groove binder; hybridisation; conjugate;
KW mismatch discrimination; diagnosis; detection; primer; probe;
KW forensic analysis; ss.
XX
OS Synthetic.
OS Enterobacteria phage M13.
XX
PN WO9951621-A2.
XX
PD 14-OCT-1999.
XX
PF 05-APR-1999; 99WO-US007487.
XX
PR 03-APR-1998; 98US-00054832.
XX
PA (EPOC-) EPOCH PHARM INC.
XX
PI Hedgpeth J, Afonina IA, Kutyavin IV, Lukhtanov EA, Belousov ES;
PI Meyer RB;
XX
DR WPI; 1999-633727/54.
XX
PT Hybridization process using oligonucleotide primer or probe that is
PT conjugated to minor groove binder, e.g. for amplification reactions or
PT assays for mutations.
XX
PS Example 1; Page 33; 95pp; English.
XX
CC A method has been developed for hybridising two nucleic acids (NA) in
CC which at least one NA comprises a minor groove binder (MGB)-
CC oligonucleotide conjugate (A). MGB is a molecule of 150-2000 D that binds
CC in a non-intercalating manner to the minor groove of a double- stranded
CC NA. Hybridisation with (A), particularly where this is a probe or primer,
CC is used: in primer extension (amplification) reactions; to identify
CC single-nucleotide (nt) mismatches; in ligase reactions; in sequencing;
CC for analysis of gene expression and detection of mutations; for detecting
CC target nucleic acids (especially for diagnosis or forensic analysis, e.g.
CC to detect human immune deficiency virus or to differentiate between its
CC subtypes, including those that are resistant to antiviral agents) and for
CC cDNA synthesis. (A) forms hybrids with complementary target sequences of
CC very high stability, so even short probes, e.g. 8-mers, are highly
CC specific and efficient. (A) also improve the discriminatory capacity of
CC short oligonucleotides, providing better detection of single-base
CC mismatches, and the speed (more rapid annealing to target) and
CC versatility of assays are increased. Short primers are easier, and less
CC expensive, to produce. The present sequence represents an oligonucleotide
CC used in an example from the present invention
XX
SQ Sequence 12 BP; 4 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 8; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12


RESULT 32
ABI33516/c
ID   ABI33516 standard; DNA; 12 BP.
XX
AC   ABI33516;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 333489 for detecting SNP TSC0037567.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 333489; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 5;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         10 AACGTTCG 3


RESULT 33
ABQ75234
ID   ABQ75234 standard; DNA; 12 BP.
XX
AC   ABQ75234;
XX
DT   05-NOV-2002  (first entry)
XX
DE   ISS immunomodulatory oligonucleotide SEQ ID NO:107.
XX
KW   Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW   allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW   idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW   malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW   immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW   virucide; antibacterial; protozoacide; ss.
XX
OS   Synthetic.
XX
PN   WO200252002-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-US050821.
XX
PR   27-DEC-2000; 2000US-0258675P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D;
XX
DR   WPI; 2002-657426/70.
XX
PT   Immunomodulatory polynucleotide for modulating an immune response in a
PT   subject suffering from disorders associated with Th2-type immune
PT   response, e.g. allergy, or infectious disease, comprises an
PT   immunostimulatory sequence.
XX
PS   Disclosure; Page 24; 95pp; English.
XX
CC   The present invention describes an immunomodulatory polynucleotide (I)
CC   comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC   immunomodulatory composition comprising (I); (2) an immunomodulatory
CC   polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC   biodegradable MC, where the MC is less than 10 micrometre in size; and
CC   (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC   antibacterial and protozoacide activities, and can be used as a modulator
CC   of immune response. (I) is useful for modulating an immune response in an
CC   individual suffering from disorders associated with a Th2-type immune
CC   response, especially an allergy or asthma, or an infectious disease. (I)
CC   is also useful for increasing interferon-gamma (IFN-gamma) in an
CC   individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC   individual having a viral infection. (I) is further useful for
CC   ameliorating a symptom of an infectious disease caused by a cellular
CC   pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC   toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC   symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC   allergy-related disorder, in particular asthma in an individual. The
CC   present sequence represents an immunomodulatory oligonucleotide from the
CC   present invention
XX
SQ   Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12


RESULT 34
ABQ75236
ID   ABQ75236 standard; DNA; 12 BP.
XX
AC   ABQ75236;
XX
DT   05-NOV-2002  (first entry)
XX
```

DE ISS immunomodulatory oligonucleotide SEQ ID NO:109.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Disclosure; Page 24; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from the
CC present invention
XX
SQ Sequence 12 BP; 2 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 8;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12
```

RESULT 35
ACA74455/c
ID ACA74455 standard; DNA; 12 BP.
XX
AC ACA74455;
XX
DT 11-AUG-2003 (first entry)
XX
DE Generated 12 nucleotide region bah.
XX
KW N_BstNBI; DNA purification; ds; site-specific nicking.
XX
OS Synthetic.
XX
PN US2003022317-A1.
XX
PD 30-JAN-2003.
XX
PF 15-DEC-2000; 2000US-00738444.
XX
PR 15-DEC-2000; 2000US-00738444.
XX
PA (NEWE) NEW ENGLAND BIOLABS INC.
XX
PI Jack WE, Schildkraut I, Menin JF;
XX
DR WPI; 2003-416989/39.
XX
PT Creating a target single-stranded region in double-stranded DNA for
PT creating expression vectors or attaching detection probes by subjecting
PT the nicked DNA to conditions where the target region is selectively
PT denatured.
XX
PS Example 8; Page 10; 34pp; English.
XX
CC The invention relates to a method of creating a target single-stranded
CC region in double-stranded DNA that comprises: (a) nicking at least one
CC site bordering the target region in double- stranded DNA with at least
CC one site-specific nicking endonuclease; and (b) subjecting the nicked DNA
CC to conditions where the target region is selectively denatured. The
CC method is useful for creating expression vectors, attaching detection
CC probes or purifying DNA molecules containing the single-stranded region.
CC The present sequence represents a generated DNA region of 18 or 12
CC nucleotides in length
XX
SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 8;  DB 7;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         11 AACGTTCG 4
```

RESULT 36
ADB88908
ID ADB88908 standard; DNA; 12 BP.
XX
AC ADB88908;
XX
DT 04-DEC-2003 (first entry)
XX
DE Chimeric immunomodulatory compound DNA sequence, SEQ ID No 111.
XX
KW chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW immunoglobulin E; IgE; allergy; cancer;
KW stimulating cellular immune system cell; ss.
XX
OS Synthetic.
XX
PN WO2003000922-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US020025.
XX
PR 21-JUN-2001; 2001US-0299883P.

PR 23-APR-2002; 2002US-0375253P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D, Tuck SF;
XX
DR WPI; 2003-210159/20.
XX
PT Novel chimeric immunomodulatory compound having immunomodulatory
PT activity, useful for modulating an immune response and for treating
PT cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS Disclosure; Page 36; 224pp; English.
XX
CC The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC having immunomodulatory activity, comprising two or more nucleic acid
CC moieties and one or more non-nucleic acid spacer moieties, where at least
CC one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC acid moieties, where the spacer is not a polypeptide, and at least one
CC nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC immunodulatory compounds more specifically contain the nucleic acid
CC spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC CIC's are useful for modulating an immune response in an individual,
CC where the individual suffers from a disorder associated with a Th2-type
CC immune response which is an allergy or allergy-induced asthma, and an
CC infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC alpha; in an individual, where the individual has idiopathic pulmonary
CC fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC disorder in an individual, where the IgE-related disorder is allergy, or
CC an allergy-related disorder. CIC's are also useful for treating cancer
CC and can be used for stimulating cellular immune system cells production
CC in an individual. This polynucleotide sequence represents a DNA sequence
CC which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC of the invention.
XX
SQ Sequence 12 BP; 2 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 8; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 5 AACGTTCG 12

RESULT 37
ADB88906
ID ADB88906 standard; DNA; 12 BP.
XX
AC ADB88906;
XX
DT 04-DEC-2003 (first entry)
XX
DE Chimeric immunomodulatory compound DNA sequence, SEQ ID No 109.
XX
KW chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW immunoglobulin E; IgE; allergy; cancer;
KW stimulating cellular immune system cell; ss.
XX
OS Synthetic.
XX
PN WO2003000922-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US020025.
XX
PR 21-JUN-2001; 2001US-0299883P.

PR 23-APR-2002; 2002US-0375253P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D, Tuck SF;
XX
DR WPI; 2003-210159/20.
XX
PT Novel chimeric immunomodulatory compound having immunomodulatory
PT activity, useful for modulating an immune response and for treating
PT cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS Disclosure; Page 36; 224pp; English.
XX
CC The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC having immunomodulatory activity, comprising two or more nucleic acid
CC moieties and one or more non-nucleic acid spacer moieties, where at least
CC one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC acid moieties, where the spacer is not a polypeptide, and at least one
CC nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC immunodulatory compounds more specifically contain the nucleic acid
CC spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC CIC's are useful for modulating an immune response in an individual,
CC where the individual suffers from a disorder associated with a Th2-type
CC immune response which is an allergy or allergy-induced asthma, and an
CC infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC alpha; in an individual, where the individual has idiopathic pulmonary
CC fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC disorder in an individual, where the IgE-related disorder is allergy, or
CC an allergy-related disorder. CIC's are also useful for treating cancer
CC and can be used for stimulating cellular immune system cells production
CC in an individual. This polynucleotide sequence represents a DNA sequence
CC which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC of the invention.
XX
SQ Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 8; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 5 AACGTTCG 12

RESULT 38
AAN70417
ID AAN70417 standard; DNA; 13 BP.
XX
AC AAN70417;
XX
DT 25-MAR-2003 (revised)
DT 16-FEB-1991 (first entry)
XX
DE Oligonucleotide forming part of human epidermal growth factor gene.
XX
KW Oligonucleotide; epidermal growth factor; fusion protein.
XX
OS Homo sapiens.
XX
PN EP234888-A.
XX
PD 02-SEP-1987.
XX
PF 20-FEB-1987; 87EP-00301490.
XX
PR 24-FEB-1986; 86US-00832337.
XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
XX
PI Cohen CM, Crea R;

```
XX
DR   WPI; 1987-244225/35.
XX
PT   Human epidermal growth factor and analogues - prepd. from a recombinant
PT   fusion protein attached through a glutamyl residue to a leader.
XX
PS   Disclosure; Page 17; 33pp; English.
XX
CC   The oligonucleotide is assembled with 25 other oligonucleotides to form
CC   the human EGF gene. This gene can be combined with other genetic elements
CC   to form the fusion protein X-Glu-EGF (X is an oligopeptide leader of up
CC   to 200 amino acids, Glu is a glutamyl residue). This protein can be
CC   selectively cleaved at the Glu residue adjacent to EGF using a Glu-
CC   specific protease without altering the Glu residues in the EGF molecule.
CC   EGF and analogues inhibit the secretion of gastric acid and promote cell
CC   growth. They are useful for wound healing and the treatment of gastric
CC   ulcers. They can also be used for the prepn. of antisera for use in
CC   immunoassays. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 13 BP; 2 A; 4 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12


RESULT 39
ABH35805/c
ID   ABH35805 standard; DNA; 13 BP.
XX
AC   ABH35805;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 235782 for detecting SNP TSC0009202.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 235782; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 6 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 5;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         10 AACGTTCG 3


RESULT 40
ABH14166/c
ID   ABH14166 standard; DNA; 13 BP.
XX
AC   ABH14166;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 214143 for detecting SNP TSC0052093.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 214143; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8;  DB 5;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
```

```
                ||||||||
Db          9 AACGTTCG 2

Search completed: April 24, 2004, 15:23:01
Job time : 117 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 15:05:43 ; Search time 23.4667 Seconds
(without alignments)
189.188 Million cell updates/sec

Title: US-09-802-445-1_COPY_9_16
Perfect score: 8
Sequence: 1 aacgttcg 8

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	8	100.0	8	4	US-09-347-343-26	Sequence 26, Appl
	2	8	100.0	8	4	US-09-347-343-30	Sequence 30, Appl
	3	8	100.0	12	4	US-09-054-832-6	Sequence 6, Appli
	4	8	100.0	12	4	US-09-640-953-6	Sequence 6, Appli
c	5	8	100.0	12	4	US-09-738-444A-42	Sequence 42, Appl
	6	8	100.0	14	3	US-09-092-314-11	Sequence 11, Appl
c	7	8	100.0	15	3	US-09-206-866-5	Sequence 5, Appli
c	8	8	100.0	15	3	US-09-206-866-6	Sequence 6, Appli
c	9	8	100.0	15	3	US-09-206-866-7	Sequence 7, Appli
c	10	8	100.0	15	3	US-09-206-866-8	Sequence 8, Appli
c	11	8	100.0	15	3	US-09-206-866-9	Sequence 9, Appli
c	12	8	100.0	15	3	US-09-206-866-10	Sequence 10, Appl
c	13	8	100.0	15	3	US-09-206-866A-5	Sequence 5, Appli
c	14	8	100.0	15	3	US-09-206-866A-6	Sequence 6, Appli
c	15	8	100.0	15	3	US-09-206-866A-7	Sequence 7, Appli
c	16	8	100.0	15	3	US-09-206-866A-8	Sequence 8, Appli
c	17	8	100.0	15	3	US-09-206-866A-9	Sequence 9, Appli
c	18	8	100.0	15	3	US-09-206-866A-10	Sequence 10, Appl
c	19	8	100.0	16	3	US-09-206-866-37	Sequence 37, Appl
c	20	8	100.0	16	3	US-09-206-866-38	Sequence 38, Appl
c	21	8	100.0	16	3	US-09-206-866-39	Sequence 39, Appl
c	22	8	100.0	16	3	US-09-206-866-40	Sequence 40, Appl
c	23	8	100.0	16	3	US-09-206-866-41	Sequence 41, Appl
c	24	8	100.0	16	3	US-09-206-866A-37	Sequence 37, Appl
c	25	8	100.0	16	3	US-09-206-866A-38	Sequence 38, Appl
c	26	8	100.0	16	3	US-09-206-866A-39	Sequence 39, Appl
c	27	8	100.0	16	3	US-09-206-866A-40	Sequence 40, Appl
c	28	8	100.0	16	3	US-09-206-866A-41	Sequence 41, Appl
	29	8	100.0	16	4	US-09-054-832-4	Sequence 4, Appli
	30	8	100.0	16	4	US-09-640-953-4	Sequence 4, Appli
c	31	8	100.0	17	3	US-09-206-866-20	Sequence 20, Appl
c	32	8	100.0	17	3	US-09-206-866-21	Sequence 21, Appl
c	33	8	100.0	17	3	US-09-206-866-22	Sequence 22, Appl
c	34	8	100.0	17	3	US-09-206-866-23	Sequence 23, Appl
c	35	8	100.0	17	3	US-09-206-866-24	Sequence 24, Appl
c	36	8	100.0	17	3	US-09-206-866A-20	Sequence 20, Appl
c	37	8	100.0	17	3	US-09-206-866A-21	Sequence 21, Appl
c	38	8	100.0	17	3	US-09-206-866A-22	Sequence 22, Appl
c	39	8	100.0	17	3	US-09-206-866A-23	Sequence 23, Appl
c	40	8	100.0	17	3	US-09-206-866A-24	Sequence 24, Appl
	41	8	100.0	20	1	US-08-255-892-37	Sequence 37, Appl
c	42	8	100.0	20	2	US-08-506-864A-11	Sequence 11, Appl
c	43	8	100.0	20	2	US-08-851-968-11	Sequence 11, Appl
c	44	8	100.0	20	3	US-09-286-098-11	Sequence 11, Appl
c	45	8	100.0	20	4	US-09-325-193A-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-09-347-343-26
; Sequence 26, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 8
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-26

Query Match 100.0%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AACGTTCG 8
              ||||||||
Db          1 AACGTTCG 8
```

RESULT 2
US-09-347-343-30
; Sequence 30, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-30

Query Match 100.0%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AACGTTCG 8
              ||||||||
Db          1 AACGTTCG 8


RESULT 3
US-09-054-832-6
; Sequence 6, Application US/09054832
; Patent No. 6312894
;  GENERAL INFORMATION:
;    APPLICANT:  Meyer, Rich
;    TITLE OF INVENTION:  IMPROVED HYBRIDIZATION AND
;    TITLE OF INVENTION:  MISMATCH DISCRIMINATION USING OLIGONUCLEOTIDES
;    TITLE OF INVENTION:  CONJUGATED TO MINOR GROOVE BINDERS
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/054,832
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/415,370
;      FILING DATE:  03-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brennan, Sean M
;      REGISTRATION NUMBER:  39,917
;      REFERENCE/DOCKET NUMBER:  34469-20004.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-054-832-6

  Query Match             100.0%;  Score 8;  DB 4;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12


RESULT 4
US-09-640-953-6
; Sequence 6, Application US/09640953
; Patent No. 6492346
;  GENERAL INFORMATION:
;       APPLICANT: Meyer, Rich
;       TITLE OF INVENTION: IMPROVED HYBRIDIZATION AND
;                           MISMATCH DISCRIMINATION USING OLIGONUCLEOTIDES
;                           CONJUGATED TO MINOR GROOVE BINDERS
;       NUMBER OF SEQUENCES: 40
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: MORRISON & FOERSTER
;            STREET: 755 PAGE MILL ROAD
;            CITY: PALO ALTO
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 94304-1018
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows
;            SOFTWARE: FastSEQ for Windows Version 2.0b
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/640,953
;            FILING DATE: 16-Aug-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/054,832
;            FILING DATE: 03-APR-1998
;            APPLICATION NUMBER: 08/415,370
;            FILING DATE: 03-APR-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brennan, Sean M
;            REGISTRATION NUMBER: 39,917
;            REFERENCE/DOCKET NUMBER: 34469-20004.20
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-813-5600
;            TELEFAX: 650-494-0792
;            TELEX: 706141
;  INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 12 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-640-953-6

  Query Match             100.0%;  Score 8;  DB 4;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12


RESULT 5
US-09-738-444A-42/c
; Sequence 42, Application US/09738444A
; Patent No. 6660475
; GENERAL INFORMATION:
;  APPLICANT: Jack, William E.
;  APPLICANT:  Schildkraut, Ira
;  APPLICANT:  Menin, Julie F.
;  APPLICANT:  Greenough, Lucia
;  TITLE OF INVENTION: Use of Site-Specific Nicking Endonucleases to Create
;  TITLE OF INVENTION:  Single-Stranded Regions And Applications Thereof
;  FILE REFERENCE: NEB-180
;  CURRENT APPLICATION NUMBER: US/09/738,444A
;  CURRENT FILING DATE:  2000-12-15
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Theoretical
;   OTHER INFORMATION: sequence - randomly generated
US-09-738-444A-42

  Query Match             100.0%;  Score 8;  DB 4;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
```

```
                ||||||||
Db         11 AACGTTCG 4


RESULT 6
US-09-092-314-11
; Sequence 11, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
;  APPLICANT:  Raz, Eyal
;  APPLICANT:  Roman, Mark
;  TITLE OF INVENTION:  Inhibitors of DNA Immunostimulatory
;  TITLE OF INVENTION:  Sequence Activity
; Patent No. 6225292
;  FILE REFERENCE:  6510-173US1
;  CURRENT APPLICATION NUMBER: US/09/092,314
;  CURRENT FILING DATE:  1998-06-05
;  PRIOR APPLICATION NUMBER:  60/048,794
;  PRIOR FILING DATE:  1997-06-06
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-09-092-314-11

  Query Match             100.0%;  Score 8;  DB 3;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          6 AACGTTCG 13


RESULT 7
US-09-206-866-5/c
; Sequence 5, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(14)
;   OTHER INFORMATION: Nucleotide 14 is n wherein n = i and i = inosine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotides 1-15 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1, 5 and 10 of the cytosine portion of cytidine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-5

  Query Match             100.0%;  Score 8;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 8
US-09-206-866-6/c
; Sequence 6, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(14)
;   OTHER INFORMATION: Nucleotide 14 is n wherein n = i and i = inosine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotides 1-15 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-6

  Query Match             100.0%;  Score 8;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 9
US-09-206-866-7/c
; Sequence 7, Application US/09206866A
; Patent No. 6150108
```

```
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(14)
;   OTHER INFORMATION: Nucleotide 14 is n wherein n = i and i = inosine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotides 1-15 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotide 1 of the cytosine portion of cytidine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-7

  Query Match             100.0%;  Score 8;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 10
US-09-206-866-8/c
; Sequence 8, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(14)
;   OTHER INFORMATION: Nucleotide 14 is n wherein n = u and u = uridine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotides 1-15 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1, 5 and 10 of the cytosine portion of cytidine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-8

  Query Match             100.0%;  Score 8;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 11
US-09-206-866-9/c
; Sequence 9, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(14)
;   OTHER INFORMATION: Nucleotide 14 is n wherein n= u and u = uridine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotides 1-15 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-9

  Query Match             100.0%;  Score 8;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
```

```
                ||||||||
Db          8 AACGTTCG 1


RESULT 12
US-09-206-866-10/c
; Sequence 10, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(14)
;   OTHER INFORMATION: Nucleotide 14 is n wherein n = u and u = uridine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotides 1-15 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotide 1 of the cytosine portion of cytidine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-10

  Query Match             100.0%;  Score 8;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
                ||||||||
Db          8 AACGTTCG 1


RESULT 13
US-09-206-866A-5/c
; Sequence 5, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(14)
;   OTHER INFORMATION: Nucleotide 14 is n wherein n = i and i = inosine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotides 1-15 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1, 5 and 10 of the cytosine portion of cytidine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-5

  Query Match             100.0%;  Score 8;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
                ||||||||
Db          8 AACGTTCG 1


RESULT 14
US-09-206-866A-6/c
; Sequence 6, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(14)
;   OTHER INFORMATION: Nucleotide 14 is n wherein n = i and i = inosine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotides 1-15 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-6

  Query Match             100.0%;  Score 8;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
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```
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 15
US-09-206-866A-7/c
; Sequence 7, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(14)
;   OTHER INFORMATION: Nucleotide 14 is n wherein n = i and i = inosine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotides 1-15 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotide 1 of the cytosine portion of cytidine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-7

  Query Match            100.0%;  Score 8;  DB 3;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 16
US-09-206-866A-8/c
; Sequence 8, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(14)
;   OTHER INFORMATION: Nucleotide 14 is n wherein n = u and u = uridine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotides 1-15 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1, 5 and 10 of the cytosine portion of cytidine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-8

  Query Match            100.0%;  Score 8;  DB 3;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 17
US-09-206-866A-9/c
; Sequence 9, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(14)
;   OTHER INFORMATION: Nucleotide 14 is n wherein n= u and u = uridine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotides 1-15 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-9

  Query Match            100.0%;  Score 8;  DB 3;  Length 15;
```

```
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 18
US-09-206-866A-10/c
; Sequence 10, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(14)
;   OTHER INFORMATION: Nucleotide 14 is n wherein n = u and u = uridine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotides 1-15 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotide 1 of the cytosine portion of cytidine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-10

  Query Match             100.0%;  Score 8;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 19
US-09-206-866-37/c
; Sequence 37, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 1-16 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine porition of
;   OTHER INFORMATION: cytidine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-37

  Query Match             100.0%;  Score 8;  DB 3;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 20
US-09-206-866-38/c
; Sequence 38, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 1-16 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotide 15 is n wherein n = i and i = inosine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-38

  Query Match             100.0%;  Score 8;  DB 3;  Length 16;
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  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 21
US-09-206-866-39/c
; Sequence 39, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 1-16 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotide 15 is n wherein n = u and u = uridine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-39

  Query Match             100.0%;  Score 8;  DB 3;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 22
US-09-206-866-40/c
; Sequence 40, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 1-16 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotide 15 is n wherein n = f and f =
;   OTHER INFORMATION: 5-fluorocytosine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-40

  Query Match             100.0%;  Score 8;  DB 3;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 23
US-09-206-866-41/c
; Sequence 41, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 1-16 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   FEATURE:
;   NAME/KEY: misc_feature
```

```
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotide 15 is n wherein n = b and b = cytosine, inosine,
;   OTHER INFORMATION: uridine, 5-bromocytidine or 5-fluorouridine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-41

  Query Match             100.0%;  Score 8;  DB 3;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 24
US-09-206-866A-37/c
; Sequence 37, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 1-16 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine porition of
;   OTHER INFORMATION: cytidine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-37

  Query Match             100.0%;  Score 8;  DB 3;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 25
US-09-206-866A-38/c
; Sequence 38, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 1-16 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotide 15 is n wherein n = i and i = inosine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-38

  Query Match             100.0%;  Score 8;  DB 3;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 26
US-09-206-866A-39/c
; Sequence 39, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 1-16 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   NAME/KEY: misc_feature
```

```
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotide 15 is n wherein n = u and u = uridine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-39

  Query Match             100.0%;  Score 8;  DB 3;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 27
US-09-206-866A-40/c
; Sequence 40, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 1-16 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotide 15 is n wherein n = f and f =
;   OTHER INFORMATION: 5-fluorocytosine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-40

  Query Match             100.0%;  Score 8;  DB 3;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 28
US-09-206-866A-41/c
; Sequence 41, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 1-16 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Nucleotide 15 is n wherein n = b and b = cytosine, inosine,
;   OTHER INFORMATION: uridine, 5-bromocytidine or 5-fluorouridine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-41

  Query Match             100.0%;  Score 8;  DB 3;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 29
US-09-054-832-4
; Sequence 4, Application US/09054832
; Patent No. 6312894
;  GENERAL INFORMATION:
;    APPLICANT:  Meyer, Rich
;    TITLE OF INVENTION:  IMPROVED HYBRIDIZATION AND
;    TITLE OF INVENTION:  MISMATCH DISCRIMINATION USING OLIGONUCLEOTIDES
;    TITLE OF INVENTION:  CONJUGATED TO MINOR GROOVE BINDERS
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/054,832
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/415,370
;      FILING DATE:  03-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brennan, Sean M
```

```
;       REGISTRATION NUMBER:  39,917
;       REFERENCE/DOCKET NUMBER:  34469-20004.20
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-813-5600
;       TELEFAX:  650-494-0792
;       TELEX:  706141
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-09-054-832-4

  Query Match             100.0%;  Score 8;  DB 4;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12


RESULT 30
US-09-640-953-4
; Sequence 4, Application US/09640953
; Patent No. 6492346
;   GENERAL INFORMATION:
;        APPLICANT: Meyer, Rich
;        TITLE OF INVENTION: IMPROVED HYBRIDIZATION AND
;                            MISMATCH DISCRIMINATION USING OLIGONUCLEOTIDES
;                            CONJUGATED TO MINOR GROOVE BINDERS
;        NUMBER OF SEQUENCES: 40
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 755 PAGE MILL ROAD
;             CITY: PALO ALTO
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304-1018
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/640,953
;             FILING DATE: 16-Aug-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/054,832
;             FILING DATE: 03-APR-1998
;             APPLICATION NUMBER: 08/415,370
;             FILING DATE: 03-APR-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brennan, Sean M
;             REGISTRATION NUMBER: 39,917
;             REFERENCE/DOCKET NUMBER: 34469-20004.20
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-813-5600
;             TELEFAX: 650-494-0792
;             TELEX: 706141
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-640-953-4

  Query Match             100.0%;  Score 8;  DB 4;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          5 AACGTTCG 12


RESULT 31
US-09-206-866-20/c
; Sequence 20, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Nucleotides 1-17 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-20

  Query Match             100.0%;  Score 8;  DB 3;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 32
US-09-206-866-21/c
; Sequence 21, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
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;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Nucleotides 1-17 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotide 16 is n wherein n = i and i = inosine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-21

  Query Match             100.0%;  Score 8;  DB 3;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 33
US-09-206-866-22/c
; Sequence 22, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Nucleotides 1-17 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotide 16 is n wherein n = u and u = uridine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-22

  Query Match             100.0%;  Score 8;  DB 3;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 34
US-09-206-866-23/c
; Sequence 23, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Nucleotides 1-17 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 12 & 16 are n wherein n = f and f =
;   OTHER INFORMATION: 5-fluorocytosine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-23

  Query Match             100.0%;  Score 8;  DB 3;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 35
US-09-206-866-24/c
; Sequence 24, Application US/09206866A
; Patent No. 6150108
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT: BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 08/653,954
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;  EARLIER FILING DATE: 1996-05-22
;  EARLIER APPLICATION NUMBER: PCT/IB97/00879
;  EARLIER FILING DATE: 1997-05-22
;  EARLIER APPLICATION NUMBER: US 60/069,812
;  EARLIER FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: US 09/194,284
;  EARLIER FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Nucleotides 1-17 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 12 & 16 are n wherein n = b and b =
;   OTHER INFORMATION: cytosine, inosine, uridine, 5-bromocytidine or
;   OTHER INFORMATION: 5-fluorouridine.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866-24

  Query Match             100.0%;  Score 8;  DB 3;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 36
US-09-206-866A-20/c
; Sequence 20, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Nucleotides 1-17 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-20

  Query Match             100.0%;  Score 8;  DB 3;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 37
US-09-206-866A-21/c
; Sequence 21, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Nucleotides 1-17 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotide 16 is n wherein n = i and i = inosine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-21

  Query Match             100.0%;  Score 8;  DB 3;  Length 17;
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  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 38
US-09-206-866A-22/c
; Sequence 22, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
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;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Nucleotides 1-17 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotide 16 is n wherein n = u and u = uridine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-22

  Query Match             100.0%;  Score 8;  DB 3;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 39
US-09-206-866A-23/c
; Sequence 23, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Nucleotides 1-17 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 12 & 16 are n wherein n = f and f =
;   OTHER INFORMATION: 5-fluorocytosine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-23

  Query Match             100.0%;  Score 8;  DB 3;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 40
US-09-206-866A-24/c
; Sequence 24, Application US/09206866A
; Patent No. 6268137
; GENERAL INFORMATION:
;  APPLICANT: SZYF, Moshe
;  APPLICANT:  BIGEY, Pascal
;  TITLE OF INVENTION: SPECIFIC INHIBITORS OF DNA METHYLTRANSFERASE
;  FILE REFERENCE: 106101.200
;  CURRENT APPLICATION NUMBER: US/09/206,866A
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 08/653,954
;  PRIOR FILING DATE: 1996-05-22
;  PRIOR APPLICATION NUMBER: PCT/IB97/00879
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/069,812
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: US 09/194,284
;  PRIOR FILING DATE: 1998-11-23
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Nucleotides 1-17 contain c, t, a & g wherein
;   OTHER INFORMATION: c=cytidine; t=thymidine; a=adenosine; g=guanosine;
;   OTHER INFORMATION: m is a methyl group at the 5-position of
;   OTHER INFORMATION: nucleotides 1 & 5 of the cytosine portion of
;   OTHER INFORMATION: cytidine.
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Nucleotides 12 & 16 are n wherein n = b and b =
;   OTHER INFORMATION: cytosine, inosine, uridine, 5-bromocytidine or
;   OTHER INFORMATION: 5-fluorouridine.
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: construct
US-09-206-866A-24

  Query Match             100.0%;  Score 8;  DB 3;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


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GenCore version 5.1.6

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Title: US-09-802-445-1_COPY_9_16
Perfect score: 8
Sequence: 1 aacgttcg 8

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	8	100.0	8	10	US-09-776-479-669	Sequence 669, App
c	3	8	100.0	8	13	US-10-314-578-669	Sequence 669, App
c	4	8	100.0	8	13	US-09-776-479-669	Sequence 669, App
	5	8	100.0	8	15	US-10-056-420-2	Sequence 2, Appli
c	6	8	100.0	8	15	US-10-112-653-642	Sequence 642, App
c	7	8	100.0	8	15	US-10-017-995-669	Sequence 669, App
	8	8	100.0	8	15	US-10-253-117-26	Sequence 26, Appl
	9	8	100.0	8	15	US-10-253-117-30	Sequence 30, Appl
	10	8	100.0	10	13	US-10-328-578-5	Sequence 5, Appli
	11	8	100.0	10	13	US-10-328-578-6	Sequence 6, Appli
	12	8	100.0	10	13	US-10-328-578-7	Sequence 7, Appli
	13	8	100.0	10	13	US-10-328-578-12	Sequence 12, Appl
	14	8	100.0	10	13	US-10-328-578-17	Sequence 17, Appl
c	15	8	100.0	10	13	US-10-328-578-17	Sequence 17, Appl
	16	8	100.0	10	13	US-10-328-578-19	Sequence 19, Appl
	17	8	100.0	10	13	US-10-328-578-20	Sequence 20, Appl
	18	8	100.0	10	13	US-10-328-578-21	Sequence 21, Appl
	19	8	100.0	10	13	US-10-328-578-22	Sequence 22, Appl
	20	8	100.0	10	15	US-10-033-243-63	Sequence 63, Appl
	21	8	100.0	10	15	US-10-033-243-64	Sequence 64, Appl
	22	8	100.0	10	15	US-10-033-243-67	Sequence 67, Appl
	23	8	100.0	10	15	US-10-033-243-72	Sequence 72, Appl
	24	8	100.0	10	15	US-10-033-243-77	Sequence 77, Appl
c	25	8	100.0	10	15	US-10-033-243-77	Sequence 77, Appl
	26	8	100.0	10	15	US-10-033-243-79	Sequence 79, Appl
	27	8	100.0	10	15	US-10-033-243-80	Sequence 80, Appl
	28	8	100.0	10	15	US-10-033-243-81	Sequence 81, Appl
	29	8	100.0	10	15	US-10-033-243-82	Sequence 82, Appl
	30	8	100.0	10	15	US-10-176-883-5	Sequence 5, Appli
	31	8	100.0	10	15	US-10-176-883-6	Sequence 6, Appli
	32	8	100.0	10	15	US-10-176-883-7	Sequence 7, Appli
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	34	8	100.0	10	15	US-10-176-883-17	Sequence 17, Appl
c	35	8	100.0	10	15	US-10-176-883-17	Sequence 17, Appl
	36	8	100.0	10	15	US-10-176-883-19	Sequence 19, Appl
	37	8	100.0	10	15	US-10-176-883-20	Sequence 20, Appl
	38	8	100.0	10	15	US-10-176-883-21	Sequence 21, Appl
	39	8	100.0	10	15	US-10-176-883-22	Sequence 22, Appl
	40	8	100.0	10	15	US-10-177-826-5	Sequence 5, Appli
	41	8	100.0	10	15	US-10-177-826-6	Sequence 6, Appli
	42	8	100.0	10	15	US-10-177-826-7	Sequence 7, Appli
	43	8	100.0	10	15	US-10-177-826-12	Sequence 12, Appl
	44	8	100.0	10	15	US-10-177-826-17	Sequence 17, Appl
c	45	8	100.0	10	15	US-10-177-826-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-888-326-185/c
; Sequence 185, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-185

Query Match 100.0%; Score 8; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+08;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 8 AACGTTCG 1

RESULT 2

US-09-776-479-669/c
; Sequence 669, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 669
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-669

Query Match 100.0%; Score 8; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+08;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 8 AACGTTCG 1

RESULT 3
US-10-314-578-669/c
; Sequence 669, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 669
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-669

Query Match 100.0%; Score 8; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+08;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 8 AACGTTCG 1

RESULT 4
US-09-776-479-669/c
; Sequence 669, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 669
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-669

Query Match 100.0%; Score 8; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+08;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 8 AACGTTCG 1

RESULT 5
US-10-056-420-2
; Sequence 2, Application US/10056420
; Publication No. US20030044428A1
; GENERAL INFORMATION:
; APPLICANT: Moss, Ronald B.
; APPLICANT: Carlo, Dennis J.
; TITLE OF INVENTION: Method For Treating an HIV-Infected
; TITLE OF INVENTION: Individual By Combining Immunization With Structured
; TITLE OF INVENTION: Interruption of Anti-Retroviral Treatment
; FILE REFERENCE: P-IM 5158
; CURRENT APPLICATION NUMBER: US/10/056,420
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/264,476
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: exemplary ISS sequence
US-10-056-420-2

Query Match 100.0%; Score 8; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+08;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 1 AACGTTCG 8

RESULT 6
US-10-112-653-642/c
; Sequence 642, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR

```
;  TITLE OF INVENTION:  TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
;  FILE REFERENCE: C01039/70060(AWS)
;  CURRENT APPLICATION NUMBER: US/10/112,653
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/279,642
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 1040
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 642
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-642

  Query Match             100.0%;  Score 8;  DB 15;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+08;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 7
US-10-017-995-669/c
; Sequence 669, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: US 60/255,534
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 669
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-017-995-669

  Query Match             100.0%;  Score 8;  DB 15;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+08;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 8
US-10-253-117-26
; Sequence 26, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
;  APPLICANT: RAZ, Eyal R.
;  APPLICANT:  KOBAYASHI, Hiroko
;  TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
;  FILE REFERENCE: 30448.64US01
;  CURRENT APPLICATION NUMBER: US/10/253,117
;  CURRENT FILING DATE:  2002-09-23
;  PRIOR APPLICATION NUMBER: US/09/347,343
;  PRIOR FILING DATE: 1999-07-02
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: synthetic oligonucleotide
US-10-253-117-26

  Query Match             100.0%;  Score 8;  DB 15;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+08;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          1 AACGTTCG 8


RESULT 9
US-10-253-117-30
; Sequence 30, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
;  APPLICANT: RAZ, Eyal R.
;  APPLICANT:  KOBAYASHI, Hiroko
;  TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
;  FILE REFERENCE: 30448.64US01
;  CURRENT APPLICATION NUMBER: US/10/253,117
;  CURRENT FILING DATE:  2002-09-23
;  PRIOR APPLICATION NUMBER: US/09/347,343
;  PRIOR FILING DATE: 1999-07-02
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: synthetic oligonucleotide
US-10-253-117-30

  Query Match             100.0%;  Score 8;  DB 15;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+08;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          1 AACGTTCG 8


RESULT 10
US-10-328-578-5
; Sequence 5, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-328-578-5
```

```
  Query Match             100.0%;  Score 8;  DB 13;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 11
US-10-328-578-6
; Sequence 6, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-328-578-6

  Query Match             100.0%;  Score 8;  DB 13;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 12
US-10-328-578-7
; Sequence 7, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-328-578-7

  Query Match             100.0%;  Score 8;  DB 13;  Length 10;
  Best Local Similarity    87.5%;  Pred. No. 4.6e+04;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||:|||
Db          3 AACGUTCG 10


RESULT 13
US-10-328-578-12
; Sequence 12, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-328-578-12

  Query Match             100.0%;  Score 8;  DB 13;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 14
US-10-328-578-17
; Sequence 17, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
```

```
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-328-578-17

  Query Match             100.0%;  Score 8;  DB 13;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 15
US-10-328-578-17/c
; Sequence 17, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-328-578-17

  Query Match             100.0%;  Score 8;  DB 13;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 16
US-10-328-578-19
; Sequence 19, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: variation
;   LOCATION: 1
;   OTHER INFORMATION: n = 5-bromocytosine
US-10-328-578-19

  Query Match             100.0%;  Score 8;  DB 13;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 17
US-10-328-578-20
; Sequence 20, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-328-578-20

  Query Match             100.0%;  Score 8;  DB 13;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 4.6e+04;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||:|||
Db          3 AACGUTCG 10
```

```
RESULT 18
US-10-328-578-21
; Sequence 21, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-328-578-21

  Query Match             100.0%;  Score 8;  DB 13;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 4.6e+04;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||:|||
Db          3 AACGUTCG 10


RESULT 19
US-10-328-578-22
; Sequence 22, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-328-578-22

  Query Match             100.0%;  Score 8;  DB 13;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 20
US-10-033-243-63
; Sequence 63, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-63

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 21
US-10-033-243-64
; Sequence 64, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-64

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10
```

```
RESULT 22
US-10-033-243-67
; Sequence 67, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-67

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 4.6e+04;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||:|||
Db          3 AACGUTCG 10


RESULT 23
US-10-033-243-72
; Sequence 72, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-72

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 24
US-10-033-243-77
; Sequence 77, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-77

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 25
US-10-033-243-77/c
; Sequence 77, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-77

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 26
US-10-033-243-79
; Sequence 79, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
```

```
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
;    LENGTH: 10
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Polynucleotide containing CG
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: 1
;    OTHER INFORMATION: n = 5-bromocytosine
US-10-033-243-79

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 27
US-10-033-243-80
; Sequence 80, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
;    LENGTH: 10
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-80

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 4.6e+04;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||:|||
Db          3 AACGUTCG 10


RESULT 28
US-10-033-243-81
; Sequence 81, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
;    LENGTH: 10
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-81

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 4.6e+04;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||:|||
Db          3 AACGUTCG 10


RESULT 29
US-10-033-243-82
; Sequence 82, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82
;    LENGTH: 10
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-82

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 30
US-10-176-883-5
; Sequence 5, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;    LENGTH: 10
;    TYPE: DNA
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-5

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 31
US-10-176-883-6
; Sequence 6, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-6

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 32
US-10-176-883-7
; Sequence 7, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-7

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 4.6e+04;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||:|||
Db          3 AACGUTCG 10


RESULT 33
US-10-176-883-12
; Sequence 12, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-12

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 34
US-10-176-883-17
; Sequence 17, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-17

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 35
US-10-176-883-17/c
; Sequence 17, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-17

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 36
US-10-176-883-19
; Sequence 19, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: variation
;   LOCATION: 1
;   OTHER INFORMATION: n = 5-bromocytosine
US-10-176-883-19

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 37
US-10-176-883-20
; Sequence 20, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-20

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 4.6e+04;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||:|||
Db          3 AACGUTCG 10


RESULT 38
US-10-176-883-21
; Sequence 21, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 10
;   TYPE: DNA
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-21

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 4.6e+04;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||:|||
Db          3 AACGUTCG 10


RESULT 39
US-10-176-883-22
; Sequence 22, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-22

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


RESULT 40
US-10-177-826-5
; Sequence 5, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-II
;  FILE REFERENCE: 377882002001
;  CURRENT APPLICATION NUMBER: US/10/177,826
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-177-826-5

  Query Match             100.0%;  Score 8;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          3 AACGTTCG 10


Search completed: April 24, 2004, 18:33:12
Job time : 107.467 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 15:03:13 ; Search time 981.867 Seconds
(without alignments)
243.309 Million cell updates/sec

Title: US-09-802-445-1_COPY_9_16
Perfect score: 8
Sequence: 1 aacgttcg 8

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	8	100.0	28	29	DME545945	AJ545945 Drosophil
c	2	8	100.0	38	29	TA335E03Q	AL492118 T. brucei
c	3	8	100.0	40	29	BX660365	BX660365 Arabidops
	4	8	100.0	45	29	BX894795	BX894795 Arabidops
	5	8	100.0	46	14	CF304811	CF304811 ABF1--06-
c	6	8	100.0	46	14	CF304811	CF304811 ABF1--06-
c	7	8	100.0	46	28	BZ355101	BZ355101 SALK_1263
c	8	8	100.0	47	28	BH865116	BH865116 SALK_0974
	9	8	100.0	48	29	BX285564	BX285564 Arabidops
	10	8	100.0	50	9	AU104223	AU104223 AU104223
c	11	8	100.0	51	29	CC884865	CC884865 SALK_1446
c	12	8	100.0	54	28	AZ300935	AZ300935 EP(2)2185
c	13	8	100.0	55	14	CF872682	CF872682 tric003xb
	14	8	100.0	55	28	AZ785311	AZ785311 2M0029E07
c	15	8	100.0	57	29	TA93B08P	AL458792 T. brucei
	16	8	100.0	58	28	BH850908	BH850908 SALK_0720
	17	8	100.0	59	9	AV966944	AV966944 AV966944
	18	8	100.0	60	12	BI550536	BI550536 603195461
c	19	8	100.0	60	12	BI550536	BI550536 603195461
c	20	8	100.0	61	29	BX289007	BX289007 Arabidops
	21	8	100.0	62	9	AU008219	AU008219 AU008219
	22	8	100.0	62	9	AU008222	AU008222 AU008222
	23	8	100.0	62	9	AU008233	AU008233 AU008233
	24	8	100.0	62	9	AU008237	AU008237 AU008237
c	25	8	100.0	63	13	BQ592229	BQ592229 E012698-0
	26	8	100.0	63	14	CF052601	CF052601 QCM5b11.y
	27	8	100.0	64	10	BE638333	BE638333 SWOvMfCAR
	28	8	100.0	64	12	BI097404	BI097404 SWOv3MCAM
	29	8	100.0	65	13	BQ667518	BQ667518 pb62f08.y
c	30	8	100.0	65	29	CG510768	CG510768 OST62667
c	31	8	100.0	65	29	CG538891	CG538891 OST129311
c	32	8	100.0	67	9	AA617006	AA617006 vk51a11.r
	33	8	100.0	67	14	CD944423	CD944423 RDI_11 Ge
c	34	8	100.0	67	29	AL761760	AL761760 Arabidops
c	35	8	100.0	68	14	CD390526	CD390526 Gm_ck0972
c	36	8	100.0	69	14	CD961219	CD961219 SDI_178 G
c	37	8	100.0	69	28	AQ025258	AQ025258 EP(3)3076
c	38	8	100.0	69	28	BZ380057	BZ380057 SALK_1145
	39	8	100.0	69	29	AL764608	AL764608 Arabidops
	40	8	100.0	69	29	AL946493	AL946493 Arabidops
	41	8	100.0	70	28	BZ382849	BZ382849 SALK_1190
c	42	8	100.0	71	10	BE024070	BE024070 sm96c11.y
c	43	8	100.0	71	14	CB025632	CB025632 TgESTzyc8
	44	8	100.0	72	29	BX127224	BX127224 Danio rer
	45	8	100.0	72	29	DR39C24S	AL974379 Danio rer

ALIGNMENTS

RESULT 1
DME545945/c
LOCUS DME545945 28 bp DNA linear GSS 24-FEB-2003
DEFINITION Drosophila melanogaster flanking sequence of RS P element insertion P{RS3}UM-8214-3, clone library P{RS3}, genomic survey sequence.
ACCESSION AJ545945
VERSION AJ545945.1 GI:28553861
KEYWORDS GSS; genome survey sequence.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1
AUTHORS Ryder,E.J., Ashburner,M., Bagunya,J., Blows,F., Bucheton,A., Coulson,D., Dickson,B., Drummond,J., Glover,D., Gunton,N., Hafen,E., Hall,S., Heisenberg,M., Lepesant,J.A., Maroy,P., Mechler,B., O'Kane,C., Pflugfelder,G., Rasmuson-Lestander,A., Reuter,G., Roote,J., Szidonya,J., Wang,S., Webster,J. and Russell,S.
TITLE Mapping of RS P element insertions in Drosophila melanogaster for the DrosDel second generation deficiency kit
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 28)
AUTHORS Ryder,E.J.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-2003) Ryder E.J., Department of Genetics,

```
            University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM
COMMENT     The insertion point of the P element is before base 1 of the
            sequence. Further information about this P element insertion line
            can be found at http://www.flyseq.org.uk and
            http://www.drosdel.org.uk.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /chromosome="3R"
                     /clone="P{RS3}UM-8214-3"
                     /clone_lib="P{RS3}"
                     /note="read=5' end"
     misc_feature    1. .28
                     /note="P element insertion in the 5' to 3' orientation"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 29;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         11 AACGTTCG 4


RESULT 2
TA335E03Q/c
LOCUS       TA335E03Q                 38 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 335e03, reverse sequence,
            genomic survey sequence.
ACCESSION   AL492118
VERSION     AL492118.1  GI:11868418
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="335e03"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 29;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         16 AACGTTCG 9


RESULT 3
BX660365/c
LOCUS       BX660365                  40 bp    DNA     linear   GSS 09-OCT-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-653E07-022839,
            genomic survey sequence.
ACCESSION   BX660365
VERSION     BX660365.1  GI:37616753
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 40)
  AUTHORS   Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-OCT-2003) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone MZF18. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-653E07-022839"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 29;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         25 AACGTTCG 18


RESULT 4
BX894795
LOCUS       BX894795                  45 bp    DNA     linear   GSS 15-DEC-2003
```

```
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-683E06-023117,
            genomic survey sequence.
ACCESSION   BX894795
VERSION     BX894795.1  GI:39927290
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 45)
  AUTHORS   Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-DEC-2003) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone MFO20. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-683E06-023117"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 29;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         22 AACGTTCG 29


RESULT 5
CF304811
LOCUS       CF304811                  46 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF1--06-A03.g1 ABF3-overexpressing transgenic rice lambda phage
            cDNA library (ABF1) Oryza sativa cDNA clone ABF1--06-A03, mRNA
            sequence.
ACCESSION   CF304811
VERSION     CF304811.1  GI:33676572
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF1--06-A03"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli SOLR"
                     /clone_lib="ABF3-overexpressing transgenic rice lambda
                     phage cDNA library (ABF1)"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; Leaf was dried for 2hrs. cDNA was inserted into
                     lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
                     with XhoI site. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
ORIGIN

  Query Match             100.0%;  Score 8;  DB 14;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         21 AACGTTCG 28


RESULT 6
CF304811/c
LOCUS       CF304811                  46 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF1--06-A03.g1 ABF3-overexpressing transgenic rice lambda phage
            cDNA library (ABF1) Oryza sativa cDNA clone ABF1--06-A03, mRNA
            sequence.
ACCESSION   CF304811
VERSION     CF304811.1  GI:33676572
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Oryza sativa"
```

```
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF1--06-A03"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli SOLR"
                     /clone_lib="ABF3-overexpressing transgenic rice lambda
                     phage cDNA library (ABF1)"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; Leaf was dried for 2hrs. cDNA was inserted into
                     lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
                     with XhoI site. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
ORIGIN

  Query Match             100.0%;  Score 8;  DB 14;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         26 AACGTTCG 19


RESULT 7
BZ355101/c
LOCUS       BZ355101                  46 bp    DNA     linear   GSS 14-NOV-2002
DEFINITION  SALK_126365.38.35.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_126365.38.35.x, genomic
            survey sequence.
ACCESSION   BZ355101
VERSION     BZ355101.1  GI:24946018
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within 300 bases of the 5' end of
            At1g61250.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_126365.38.35.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 28;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         35 AACGTTCG 28


RESULT 8
BH865116/c
LOCUS       BH865116                  47 bp    DNA     linear   GSS 05-AUG-2002
DEFINITION  SALK_097417 Arabidopsis thaliana TDNA insertion lines Arabidopsis
            thaliana genomic clone SALK_097417, genomic survey sequence.
ACCESSION   BH865116
VERSION     BH865116.1  GI:22101014
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At3g57980.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_097417"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 28;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          9 AACGTTCG 2


RESULT 9
BX285564
LOCUS       BX285564                  48 bp    DNA     linear   GSS 07-MAR-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-383G05-017270,
            genomic survey sequence.
ACCESSION   BX285564
VERSION     BX285564.1  GI:28884560
KEYWORDS    GSS.
```

```
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 48)
  AUTHORS   Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-2003) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone f15b18.
            The sequences are generated at the MPI for Plant Breeding Research
            in the context of the GABI-Kat project. GABI-Kat is part of the
            German Plant Genomics program designated 'GABI'. Information on
            line availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-383G05-017270"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 29;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         13 AACGTTCG 20


RESULT 10
AU104223
LOCUS       AU104223                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU104223 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HEP21349, mRNA sequence.
ACCESSION   AU104223
VERSION     AU104223.1  GI:13553744
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
  PUBMED    11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HEP21349"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         25 AACGTTCG 32


RESULT 11
CC884865/c
LOCUS       CC884865                 51 bp    DNA     linear   GSS 31-JUL-2003
DEFINITION  SALK_144687.15.95.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_144687.15.95.x, genomic
            survey sequence.
ACCESSION   CC884865
VERSION     CC884865.1  GI:33361221
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within 300 bases of the 3' end of
            At5g37130.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_144687.15.95.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
```

each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 100.0%; Score 8; DB 29; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AACGTTCG 8
              ||||||||
Db         33 AACGTTCG 26
```

RESULT 12
AZ300935/c
LOCUS AZ300935 54 bp DNA linear GSS 23-AUG-2000
DEFINITION EP(2)2185 Drosophila melanogaster EP line Drosophila melanogaster genomic Both 5' and 3' ends of P element, genomic survey sequence.
ACCESSION AZ300935
VERSION AZ300935.1 GI:9650436
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 54)
AUTHORS Liao,G.-C., Rehm,E.J. and Rubin,G.M.
TITLE Insertion site preferences of the P transposable element in Drosophila melanogaster
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
MEDLINE 20202638
PUBMED 10716700
COMMENT Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P element

The P element insertion position is base 1 in the 54 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
Class: transposon-tagged.

FEATURES Location/Qualifiers
source 1. .54
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster EP line"
/note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains a single EP transposable element insertion. (The generation of these insertion strains is described in Rorth P, Szabo K, Bailey A, Laverty T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes V, Ansorge W, Cohen SM. 1998. Systematic gain-of-function genetics in Drosophila. Development 6:1049-1057.) The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."

ORIGIN

Query Match 100.0%; Score 8; DB 28; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AACGTTCG 8
              ||||||||
Db         19 AACGTTCG 12
```

RESULT 13
CF872682/c
LOCUS CF872682 55 bp mRNA linear EST 31-OCT-2003
DEFINITION tric003xb03.b11 T.reesei mycelial culture, Version 6 October 2003 Hypocrea jecorina cDNA clone tric003xb03, mRNA sequence.
ACCESSION CF872682
VERSION CF872682.1 GI:38127364
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE 1 (bases 1 to 55)
AUTHORS Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D., Mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward,M. and Dean,R.A.
TITLE Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset
JOURNAL Unpublished (2003)
COMMENT Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph_dean@ncsu.edu
Seq primer: LT-F1 primer.

FEATURES Location/Qualifiers
source 1. .55
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric003xb03"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October 2003"
/note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN

Query Match 100.0%; Score 8; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AACGTTCG 8
              ||||||||
Db         14 AACGTTCG 7
```

RESULT 14
AZ785311
LOCUS AZ785311 55 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0029E07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0029E07 F, genomic survey sequence.
ACCESSION AZ785311
VERSION AZ785311.1 GI:12921925
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 55)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

```
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0029  row: E  column: 07
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 55.
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0029E07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             100.0%;  Score 8;  DB 28;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         35 AACGTTCG 42


RESULT 15
TA93B08P/c
LOCUS       TA93B08P                  57 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 93b08, forward sequence,
            genomic survey sequence.
ACCESSION   AL458792
VERSION     AL458792.1  GI:11861264
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 57)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .57
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="93b08"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 29;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         48 AACGTTCG 41


RESULT 16
BH850908
LOCUS       BH850908                  58 bp    DNA     linear   GSS 13-JUN-2002
DEFINITION  SALK_072062.19.60.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_072062.19.60.x, genomic
            survey sequence.
ACCESSION   BH850908
VERSION     BH850908.1  GI:21421779
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 58)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At4g21110.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .58
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_072062.19.60.x"
```

/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 100.0%; Score 8; DB 28; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 30 AACGTTCG 37

RESULT 17
AV966944
LOCUS AV966944 59 bp mRNA linear EST 14-MAR-2002
DEFINITION AV966944 Nori Satoh unpublished cDNA library, young adult Ciona intestinalis cDNA clone ciad20118 5', mRNA sequence.
ACCESSION AV966944
VERSION AV966944.1 GI:19456640
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 59)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .59
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="ciad20118"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"

ORIGIN

Query Match 100.0%; Score 8; DB 9; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 12 AACGTTCG 19

RESULT 18
BI550536
LOCUS BI550536 60 bp mRNA linear EST 05-SEP-2001
DEFINITION 603195461F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5275095 5', mRNA sequence.
ACCESSION BI550536
VERSION BI550536.1 GI:15437848
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 60)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11694 row: i column: 16
High quality sequence stop: 60.
FEATURES Location/Qualifiers
source 1. .60
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5275095"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 8; DB 12; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 43 AACGTTCG 50

RESULT 19
BI550536/c
LOCUS BI550536 60 bp mRNA linear EST 05-SEP-2001
DEFINITION 603195461F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5275095 5', mRNA sequence.
ACCESSION BI550536
VERSION BI550536.1 GI:15437848
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 60)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

```
           Plate: LLAM11694  row: i  column: 16
           High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5275095"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_95"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.5 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this
                     is a NIH_MGC Library."
ORIGIN

  Query Match             100.0%;  Score 8;  DB 12;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         48 AACGTTCG 41


RESULT 20
BX289007/c
LOCUS       BX289007                61 bp    DNA     linear   GSS 07-MAR-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-422E01-017846,
            genomic survey sequence.
ACCESSION   BX289007
VERSION     BX289007.1  GI:28888003
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 61)
  AUTHORS   Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-2003) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion close to or within gene At5g16100. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .61
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-422E01-017846"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 29;  Length 61;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db          8 AACGTTCG 1


RESULT 21
AU008219
LOCUS       AU008219                62 bp    mRNA    linear   EST 31-JUL-1998
DEFINITION  AU008219 Schizosaccharomyces pombe late log phase cDNA
            Schizosaccharomyces pombe cDNA clone spc03066, mRNA sequence.
ACCESSION   AU008219
VERSION     AU008219.1  GI:3344677
KEYWORDS    EST.
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 62)
  AUTHORS   Morimyo,M. and Mita,K.
  TITLE     Identification of expressed sequence tags of Schizosaccharomyces
            pombe
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Mitsuoki Morimyo
            Genome Research Group
            National Institute of Radiological Sciences
            9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
            Email: morimyo@nirs.go.jp.
FEATURES             Location/Qualifiers
     source          1. .62
                     /organism="Schizosaccharomyces pombe"
                     /mol_type="mRNA"
                     /strain="972"
                     /db_xref="taxon:4896"
                     /clone="spc03066"
                     /sex="h minus"
                     /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                     /note="Vector: M13mp19; The cDNA library of
                     Schizosaccharomyces pombe was prepared by cloning cDNA
                     into the SmaI site of M13mp19 DNA and the direction of DNA
                     sequences was not always from 5' to 3'. The cDNA data of
                     Schizosaccharomyces pombe are available for searching on
                     the World Wide Web.  (URL, http://www.nirs.go.jp)"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 9;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         32 AACGTTCG 39
```

```
RESULT 22
AU008222
LOCUS       AU008222                 62 bp    mRNA    linear   EST 31-JUL-1998
DEFINITION  AU008222 Schizosaccharomyces pombe late log phase cDNA
            Schizosaccharomyces pombe cDNA clone spc03071, mRNA sequence.
ACCESSION   AU008222
VERSION     AU008222.1  GI:3344680
KEYWORDS    EST.
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 62)
  AUTHORS   Morimyo,M. and Mita,K.
  TITLE     Identification of expressed sequence tags of Schizosaccharomyces
            pombe
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Mitsuoki Morimyo
            Genome Research Group
            National Institute of Radiological Sciences
            9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
            Email: morimyo@nirs.go.jp.
FEATURES             Location/Qualifiers
     source          1. .62
                     /organism="Schizosaccharomyces pombe"
                     /mol_type="mRNA"
                     /strain="972"
                     /db_xref="taxon:4896"
                     /clone="spc03071"
                     /sex="h minus"
                     /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                     /note="Vector: M13mp19; The cDNA library of
                     Schizosaccharomyces pombe was prepared by cloning cDNA
                     into the SmaI site of M13mp19 DNA and the direction of DNA
                     sequences was not always from 5' to 3'. The cDNA data of
                     Schizosaccharomyces pombe are available for searching on
                     the World Wide Web.  (URL, http://www.nirs.go.jp)"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 9;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         32 AACGTTCG 39


RESULT 23
AU008233
LOCUS       AU008233                 62 bp    mRNA    linear   EST 31-JUL-1998
DEFINITION  AU008233 Schizosaccharomyces pombe late log phase cDNA
            Schizosaccharomyces pombe cDNA clone spc03087, mRNA sequence.
ACCESSION   AU008233
VERSION     AU008233.1  GI:3344691
KEYWORDS    EST.
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 62)
  AUTHORS   Morimyo,M. and Mita,K.
  TITLE     Identification of expressed sequence tags of Schizosaccharomyces
            pombe
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Mitsuoki Morimyo
            Genome Research Group
            National Institute of Radiological Sciences
            9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
            Email: morimyo@nirs.go.jp.
FEATURES             Location/Qualifiers
     source          1. .62
                     /organism="Schizosaccharomyces pombe"
                     /mol_type="mRNA"
                     /strain="972"
                     /db_xref="taxon:4896"
                     /clone="spc03087"
                     /sex="h minus"
                     /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                     /note="Vector: M13mp19; The cDNA library of
                     Schizosaccharomyces pombe was prepared by cloning cDNA
                     into the SmaI site of M13mp19 DNA and the direction of DNA
                     sequences was not always from 5' to 3'. The cDNA data of
                     Schizosaccharomyces pombe are available for searching on
                     the World Wide Web.  (URL, http://www.nirs.go.jp)"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 9;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         32 AACGTTCG 39


RESULT 24
AU008237
LOCUS       AU008237                 62 bp    mRNA    linear   EST 31-JUL-1998
DEFINITION  AU008237 Schizosaccharomyces pombe late log phase cDNA
            Schizosaccharomyces pombe cDNA clone spc03091, mRNA sequence.
ACCESSION   AU008237
VERSION     AU008237.1  GI:3344695
KEYWORDS    EST.
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 62)
  AUTHORS   Morimyo,M. and Mita,K.
  TITLE     Identification of expressed sequence tags of Schizosaccharomyces
            pombe
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Mitsuoki Morimyo
            Genome Research Group
            National Institute of Radiological Sciences
            9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
            Email: morimyo@nirs.go.jp.
FEATURES             Location/Qualifiers
     source          1. .62
                     /organism="Schizosaccharomyces pombe"
                     /mol_type="mRNA"
                     /strain="972"
                     /db_xref="taxon:4896"
                     /clone="spc03091"
                     /sex="h minus"
                     /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                     /note="Vector: M13mp19; The cDNA library of
                     Schizosaccharomyces pombe was prepared by cloning cDNA
                     into the SmaI site of M13mp19 DNA and the direction of DNA
                     sequences was not always from 5' to 3'. The cDNA data of
                     Schizosaccharomyces pombe are available for searching on
                     the World Wide Web.  (URL, http://www.nirs.go.jp)"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 9;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         32 AACGTTCG 39
```

```
RESULT 25
BQ592229/c
LOCUS       BQ592229                 63 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  EO12698-024-021-D22-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-021-D22 5-PRIME, mRNA sequence.
ACCESSION   BQ592229
VERSION     BQ592229.1  GI:26121812
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 63)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 63   Std Error: 0.00
            Plate: 21  row: D  column: 22
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .63
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:190741"
                     /db_xref="taxon:161934"
                     /clone="024-021-D22"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 13;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         55 AACGTTCG 48


RESULT 26
CF052601
LOCUS       CF052601                 63 bp    mRNA    linear   EST 21-JUL-2003
DEFINITION  QCM5b11.yg QCM Zea mays cDNA clone QCM5b11, mRNA sequence.
ACCESSION   CF052601
VERSION     CF052601.1  GI:33092607
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 63)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .63
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="F2"
                     /db_xref="taxon:4577"
                     /clone="QCM5b11"
                     /tissue_type="apex"
                     /clone_lib="QCM"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 14;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         56 AACGTTCG 63


RESULT 27
BE638333
LOCUS       BE638333                 64 bp    mRNA    linear   EST 28-AUG-2000
DEFINITION  SWOvMfCAR18A08SK Onchocerca volvulus microfilaria cDNA
            (SAW98MLW-OvMf) Onchocerca volvulus cDNA clone SWOvMfCAR18A08 5',
            mRNA sequence.
ACCESSION   BE638333
VERSION     BE638333.1  GI:9937035
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in microfilaria of Onchocerca volvulus
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6282"
                     /clone="SWOvMfCAR18A08"
                     /dev_stage="microfilaria"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus microfilaria cDNA
                     (SAW98MLW-OvMf)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
```

Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 200,000 microfilariae isolated from the skin of infected individuals from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.8 x 10E4 independent recombinants and the average insert size is approximately 1kb. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email:genome@smith.edu."

ORIGIN

Query Match 100.0%; Score 8; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 5 AACGTTCG 12

RESULT 28
BI097404
LOCUS BI097404 64 bp mRNA linear EST 25-JUN-2001
DEFINITION SWOv3MCAM63D09SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM63D09 5', mRNA sequence.
ACCESSION BI097404
VERSION BI097404.1 GI:14549061
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 64)
AUTHORS Williams,S.A., Lizotte-Waniewski,M., Laney,S. and Lustigman,S.
TITLE Genes expressed in molting L3 larvae of Onchocerca volvulus
JOURNAL Unpublished (1997)
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .64
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone="SWOv3MCAM63D09"
/dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."

ORIGIN

Query Match 100.0%; Score 8; DB 12; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGTTCG 8
||||||||
Db 16 AACGTTCG 23

RESULT 29
BQ667518
LOCUS BQ667518 65 bp mRNA linear EST 15-JUL-2002
DEFINITION pb62f08.y1 Anc caninum L3 serum stim pAMP1 v1 Chiapelli McCarter Ancylostoma caninum cDNA 5', mRNA sequence.
ACCESSION BQ667518
VERSION BQ667518.1 GI:21809200
KEYWORDS EST.
SOURCE Ancylostoma caninum (dog hookworm)
ORGANISM Ancylostoma caninum
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
REFERENCE 1 (bases 1 to 65)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis. Nematodes were provided by Dr. Prema Arasu of North Carolina State University.
Putative full length read
The vector to vector length is 66.
FEATURES Location/Qualifiers
source 1. .65
/organism="Ancylostoma caninum"
/mol_type="mRNA"
/db_xref="taxon:29170"
/dev_stage="serum stimulated L3"
/lab_host="DH10B"
/clone_lib="Anc caninum L3 serum stim pAMP1 v1 Chiapelli McCarter"
/note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI; The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. Prema Arasu of North Carolina State University."

ORIGIN

Query Match 100.0%; Score 8; DB 13; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AACGTTCG 8
              ||||||||
Db         38 AACGTTCG 45


RESULT 30
CG510768/c
LOCUS       CG510768                  65 bp    DNA     linear   GSS 01-OCT-2003
DEFINITION  OST62667 Mus musculus 129Sv/Ev Mus musculus genomic clone OST62667,
            genomic survey sequence.
ACCESSION   CG510768
VERSION     CG510768.1  GI:37295352
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129SV/EV"
                     /db_xref="taxon:10090"
                     /clone="OST62667"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 29;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         33 AACGTTCG 26


RESULT 31
CG538891/c
LOCUS       CG538891                  65 bp    DNA     linear   GSS 01-OCT-2003
DEFINITION  OST129311 Mus musculus 129Sv/Ev Mus musculus genomic clone
            OST129311, genomic survey sequence.
ACCESSION   CG538891
VERSION     CG538891.1  GI:37325463
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129SV/EV"
                     /db_xref="taxon:10090"
                     /clone="OST129311"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 29;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         33 AACGTTCG 26


RESULT 32
AA617006/c
LOCUS       AA617006                  67 bp    mRNA    linear   EST 07-OCT-1997
DEFINITION  vk51a11.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
            IMAGE:958172 5' similar to gb:U12403 Mus musculus Csa-19 mRNA,
            complete cds (MOUSE);, mRNA sequence.
ACCESSION   AA617006
VERSION     AA617006.1  GI:2504211
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 67)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:546964
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .67
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:958172"
```

```
                     /tissue_type="Tcell"
                     /dev_stage="M30 CD4+ cells"
                     /lab_host="SOLR (kanamycin resistant)"
                     /clone_lib="Stratagene mouse Tcell 937311"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 9;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         66 AACGTTCG 59


RESULT 33
CD944423
LOCUS       CD944423                  67 bp    mRNA    linear   EST 15-JUL-2003
DEFINITION  RDI_11 GeneTag1 Zea mays cDNA, mRNA sequence.
ACCESSION   CD944423
VERSION     CD944423.1  GI:32792187
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 67)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .67
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="mixture"
                     /db_xref="taxon:4577"
                     /clone_lib="GeneTag1"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 14;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         14 AACGTTCG 21


RESULT 34
AL761760/c
LOCUS       AL761760                  67 bp    DNA     linear   GSS 18-JUN-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-228B04-014263,
            genomic survey sequence.
ACCESSION   AL761760
VERSION     AL761760.1  GI:21505120
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 67)
  AUTHORS   Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone T6C23. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .67
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-228B04-014263"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 29;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         23 AACGTTCG 16


RESULT 35
CD390526/c
LOCUS       CD390526                  68 bp    mRNA    linear   EST 01-JUN-2003
DEFINITION  Gm_ck0972 Soybean induced by Salicylic Acid Glycine max cDNA 3',
            mRNA sequence.
ACCESSION   CD390526
VERSION     CD390526.1  GI:31305323
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 68)
  AUTHORS   Tian,A.-G., Wang,J., Cui,P., Han,Y.-J., Xu,H., Cong,L.-J.,
            Huang,X.-G., Wang,X.-L., Jiao,Y.-Z., Wang,B.-J., Wang,Y.-J.,
            Zhang,J.-S., Chen,S.-Y. and Yu,J.
  TITLE     Soybean Expressed Sequence Tags Sequencing
```

```
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Chen S-Y
            Plant Biotechnology Laboratory
            Institute of Genetics and Developmental Biology, CAS, China
            Datun road, Beijing 100101, China
            Tel: 86-10-64886859
            Fax: 86-10-64873428
            Email: sychen@genetics.ac.cn
            Email: sychen@genetics.ac.cn
            Seq primer: T7 primer.
FEATURES             Location/Qualifiers
     source          1. .68
                     /organism="Glycine max"
                     /mol_type="mRNA"
                     /cultivar="Kefeng 1"
                     /db_xref="taxon:3847"
                     /tissue_type="Seedlings"
                     /dev_stage="two-week seedlings"
                     /lab_host="XL1-Blue MRF' strain"
                     /clone_lib="Soybean induced by Salicylic Acid"
                     /note="Vector: pBluescript SK+; Site_1: EcoR I; Site_2:
                     Xho I; The cDNA library was constructed by He, C-Y from
                     mRNA isolated from two-week seedlings (cultivar Kefeng 1)
                     treated by spraying 2.0mM salicylic acid for 24, 36, 48
                     and 72 h. Complementary DNA was synthesized from mRNA
                     using a primer consisting of a poly(dT) sequence with a
                     XhoI striction site. EcoRI adapters were ligated to the
                     blunt-ended cDNA fragments followed by XhoI digestion. The
                     cDNA fragments were directionally cloned into the
                     EcoRI-XhoI restriction site of the pBluescript vector. The
                     ligated cDNA fragments were transformed into XL1-Blue MRF'
                     host cells (Stratagene)."
ORIGIN

  Query Match             100.0%;  Score 8;  DB 14;  Length 68;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         45 AACGTTCG 38


RESULT 36
CD961219/c
LOCUS       CD961219                  69 bp    mRNA    linear   EST 15-JUL-2003
DEFINITION  SDI_178 GeneTag2 Zea mays cDNA, mRNA sequence.
ACCESSION   CD961219
VERSION     CD961219.1  GI:32808985
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 69)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .69
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="mixture"
                     /db_xref="taxon:4577"
                     /clone_lib="GeneTag2"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 14;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         68 AACGTTCG 61


RESULT 37
AQ025258/c
LOCUS       AQ025258                  69 bp    DNA     linear   GSS 23-AUG-2000
DEFINITION  EP(3)3076 Drosophila melanogaster EP line Drosophila melanogaster
            genomic Sequence recovered from 5' end of P element, genomic survey
            sequence.
ACCESSION   AQ025258
VERSION     AQ025258.1  GI:3265610
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 69)
  AUTHORS   Liao,G.-C., Rehm,E.J. and Rubin,G.M.
  TITLE     Insertion site preferences of the P transposable element in
            Drosophila melanogaster
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
  MEDLINE   20202638
   PUBMED   10716700
COMMENT     Contact: Gerald Rubin
            Berkeley Drosophila Genome Project
            University of California, Berkeley
            LSA Building, Berkeley, CA 94720-3200, USA
            Fax: 5106439947
            Email: gerry@fruitfly.berkeley.edu
            Sequence recovery method was inverse PCR.

            Sequence orientation is forward strand relative to 5' end of P
            element

            The P element insertion position is base 62 in the 69 bases. This
            insertion position refers to the first base of the 8 base target
            recognition sequence.
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .69
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone_lib="Drosophila melanogaster EP line"
                     /note="Inverse PCR was performed on Drosophila
                     melanogaster strains each of which contains a single EP
                     transposable element insertion. (The generation of these
                     insertion strains is described in Rorth P, Szabo K, Bailey
                     A, Laverty T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes
                     V, Ansorge W, Cohen SM. 1998. Systematic gain-of-function
                     genetics in Drosophila. Development 6:1049-1057.) The
                     resultant fragment for each strain was directly sequenced
                     to determine the genomic sequence at the site of
                     insertion. Details of the protocols used can be found at
                     http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."
ORIGIN

  Query Match             100.0%;  Score 8;  DB 28;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
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Db         40 AACGTTCG 33


RESULT 38
BZ380057/c
LOCUS       BZ380057                 69 bp    DNA     linear   GSS 26-NOV-2002
DEFINITION  SALK_114531.36.25.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_114531.36.25.x, genomic
            survey sequence.
ACCESSION   BZ380057
VERSION     BZ380057.1  GI:25472531
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 69)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within 300 bases of the 5' end of
            At2g20560.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .69
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_114531.36.25.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match           100.0%;  Score 8;  DB 28;  Length 69;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         59 AACGTTCG 52


RESULT 39
AL764608
LOCUS       AL764608                 69 bp    DNA     linear   GSS 18-JUN-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-128F09-012669,
            genomic survey sequence.
ACCESSION   AL764608
VERSION     AL764608.1  GI:21517651
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 69)
  AUTHORS   Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone F4P13. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .69
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-128F09-012669"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
ORIGIN

  Query Match           100.0%;  Score 8;  DB 29;  Length 69;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         33 AACGTTCG 40


RESULT 40
AL946493
LOCUS       AL946493                 69 bp    DNA     linear   GSS 30-NOV-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-297A04-015513,
            genomic survey sequence.
ACCESSION   AL946493
VERSION     AL946493.1  GI:24403115
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
```

```
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 69)
  AUTHORS   Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone f15b18.
            The sequences are generated at the MPI for Plant Breeding Research
            in the context of the GABI-Kat project. GABI-Kat is part of the
            German Plant Genomics program designated 'GABI'. Information on
            line availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .69
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-297A04-015513"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
ORIGIN

  Query Match             100.0%;  Score 8;  DB 29;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACGTTCG 8
              ||||||||
Db         23 AACGTTCG 30


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